



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 125396**

**TO: Fozia Hamud**  
**Location: 4d64 / 4c70**  
**Thursday, June 24, 2004**  
**Art Unit: 1647**  
**Phone: 272-0884**  
**Serial Number: 10 / 015393**

**From: Jan Delaval**  
**Location: Biotech-Chem Library**  
**Rem 1A51**  
**Phone: 272-2504**  
**jan.delaval@uspto.gov**

### **Search Notes**

125396

STIC-Biotech/ChemLib

From: Chan, Christina  
Sent: Wednesday, June 23, 2004 8:23 AM  
To: Hamud, Fozia; STIC-Biotech/ChemLib  
Subject: RE: rush search

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 & 1642  
(571)-272-0841  
Remsen, 3E89

-----Original Message-----

From: Hamud, Fozia  
Sent: Wednesday, June 23, 2004 7:56 AM  
To: Chan, Christina  
Subject: rush search

Hi Christina, 10/015,393 is a date case that I must finish this bi-week. Would you kindly approve this rush search.  
Thank you very much.

Stic,

Please search SEQ ID NOs: 115 and 116 of 10/015,393 against commercial and interference data bases.

Fozia Hamud  
Patent Examiner  
Art Unit 1647  
Remsen: Room 4D64  
Mail box: Remsen 4C70  
272-0884

Searcher: [Signature]  
Phone: 22504  
Location: \_\_\_\_\_  
Date Picked Up: 6/23  
Date Completed: 6/24  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: 20  
Online time: 20

TYPE OF SEARCH:  
NA Sequences: ✓  
AA Sequences: ✓  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: ✓  
Sequence Sys.: ✓  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2004, 11:04:51 ; Search time 735 Seconds  
(without alignments)  
10449.989 Million cell updates/sec

Title: US-10-015-393A-115  
Perfect score: 1808  
Sequence: 1 gagctaccaggcggtgtt.....actctcaacttgcattt 1808

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1808	100.0	1808	3	AAA37054	Aaa37054 Human PRO
2	1808	100.0	1808	4	AAF54284	Aaf54284 DNA encod
3	1808	100.0	1808	8	ACD68321	Acd68321 Novel hum
4	1808	100.0	1808	8	ACH04423	Ach04423 Human cdn
5	1808	100.0	1808	8	ACD67967	Acd67967 Novel hum
6	1808	100.0	1808	9	ADC17984	Adc17984 Human PRO
7	1808	100.0	1808	9	ADD70630	Add70630 Human cdn
8	1808	100.0	1808	9	ADD39707	Add39707 Human cdn
9	1808	100.0	1808	9	ADD70153	Add70153 Human cdn
10	1808	100.0	1808	9	ADD38274	Add38274 Human cdn
11	1808	100.0	1808	9	ADD39230	Add39230 Human cdn
12	1808	100.0	1808	9	ADD38753	Add38753 Human cdn
13	1808	100.0	1808	9	ADD40184	Add40184 Human cdn
14	1808	100.0	1808	9	ADE50405	Ade50405 Human cdn
15	1808	100.0	1808	9	ADE20017	Ade20017 Human cdn
16	1808	100.0	1808	9	ADE49928	Ade49928 Human cdn
17	1808	100.0	1808	9	ADE21486	Ade21486 Human cdn
18	1799.2	99.5	2069	8	AAD56357	Aad56357 Human sec
19	1792	99.1	1878	5	AAF93783	Aaf93783 Human cdn
20	1231.4	68.1	1282	4	AAD09940	Aad09940 Human dru
21	1189.8	65.8	1699	4	AAH25133	Aah25133 Nucleotid
22	1189.8	65.8	1699	6	ABK15714	Abk15714 Human 216
23	1150.2	63.6	1195	6	ABK35374	Abk35374 Human cdn

C	24	1098.6	60.8	1235	5	AAD07737	Aad07737 Human sec
	25	1037.4	57.4	1167	4	AAI59543	Aai59543 Human pol
	26	966.4	53.5	2593	4	AAK71133	Aak71133 Human imm
	27	963.2	53.3	2590	4	AAK71135	Aak71135 Human imm
C	28	935.8	51.8	1668	4	AAI61329	Aai61329 Human pol
	29	916.8	50.7	1153	4	AAH25132	Aah25132 Nucleotid
	30	916.8	50.7	1153	6	ABK15713	Abk15713 Human 337
	31	824.4	45.6	4787	5	AAS92566	Aas92566 DNA encod
	32	739.2	40.9	847	3	AAF16282	Aaf16282 Human pro
	33	737.6	40.8	847	4	AAD05504	Aad05504 Human sec
	34	737.6	40.8	847	5	AAD07712	Aad07712 Human sec
	35	622.8	34.4	1698	6	AAS62643	Aas62643 cDNA sequ
	36	525.2	29.0	556	5	AAS79599	Aas79599 DNA encod
C	37	500	27.7	554	5	AAF94126	Aaf94126 Primer sp
	38	473.8	26.2	553	6	ABN60026	Abn60026 Novel hum
C	39	456.4	25.2	726	5	AAS66868	Aas66868 DNA encod
	40	391.2	21.6	400	5	AAS92563	Aas92563 DNA encod
	41	373	20.6	477	5	AAF93979	Aaf93979 Primer sp
C	42	337.2	18.7	890	5	AAS29534	Aas29534 Human end
	43	297.8	16.5	2494	4	AAD10112	Aad10112 Rat secre
	44	297.8	16.5	2494	6	ABL35027	Ab135027 Rat cDNA
	45	271.6	15.0	904	4	ABL04019	Ab104019 Drosophil

ALIGNMENTS

RESULT 1  
AAA37054  
ID AAA37054 standard; cDNA; 1808 BP.  
XX  
AC AAA37054;  
XX  
DT 08-AUG-2000 (first entry)  
XX  
DE Human PRO1430 (UNQ736) cDNA sequence SEQ ID NO:115.  
XX  
KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;  
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200012708-A2.  
XX  
PD 09-MAR-2000.  
XX  
PF 01-SEP-1999; 99WO-US020111.  
XX

Result No. Score Query Match Length DB ID Description

PR 16-SEP-1998; 98US-0100662P.  
PR 16-SEP-1998; 98US-0100664P.  
PR 17-SEP-1998; 98US-0100683P.  
PR 17-SEP-1998; 98US-0100684P.  
PR 17-SEP-1998; 98US-0100710P.  
PR 17-SEP-1998; 98US-0100711P.  
PR 17-SEP-1998; 98US-0100919P.  
PR 17-SEP-1998; 98US-0100930P.  
PR 18-SEP-1998; 98US-0100848P.  
PR 18-SEP-1998; 98US-0100849P.  
PR 18-SEP-1998; 98US-0101014P.  
PR 18-SEP-1998; 98US-0101068P.  
PR 18-SEP-1998; 98US-0101071P.  
PR 22-SEP-1998; 98US-0101279P.  
PR 23-SEP-1998; 98US-0101471P.  
PR 23-SEP-1998; 98US-0101472P.  
PR 23-SEP-1998; 98US-0101474P.  
PR 23-SEP-1998; 98US-0101475P.  
PR 23-SEP-1998; 98US-0101476P.  
PR 23-SEP-1998; 98US-0101477P.  
PR 23-SEP-1998; 98US-0101479P.  
PR 24-SEP-1998; 98US-0101738P.  
PR 24-SEP-1998; 98US-0101741P.  
PR 24-SEP-1998; 98US-0101743P.  
PR 24-SEP-1998; 98US-0101915P.  
PR 24-SEP-1998; 98US-0101916P.  
PR 29-SEP-1998; 98US-0102207P.  
PR 29-SEP-1998; 98US-0102240P.  
PR 29-SEP-1998; 98US-0102307P.  
PR 29-SEP-1998; 98US-0102330P.  
PR 29-SEP-1998; 98US-0102331P.  
PR 30-SEP-1998; 98US-0102484P.  
PR 30-SEP-1998; 98US-0102487P.  
PR 30-SEP-1998; 98US-0102570P.  
PR 30-SEP-1998; 98US-0102571P.  
PR 01-OCT-1998; 98US-0102684P.  
PR 01-OCT-1998; 98US-0102687P.  
PR 02-OCT-1998; 98US-0102965P.  
PR 06-OCT-1998; 98US-0103258P.  
PR 06-OCT-1998; 98US-0103449P.  
PR 07-OCT-1998; 98US-0103314P.  
PR 07-OCT-1998; 98US-0103315P.  
PR 07-OCT-1998; 98US-0103328P.  
PR 07-OCT-1998; 98US-0103395P.  
PR 07-OCT-1998; 98US-0103396P.  
PR 07-OCT-1998; 98US-0103401P.  
PR 08-OCT-1998; 98US-0103633P.  
PR 08-OCT-1998; 98US-0103678P.  
PR 08-OCT-1998; 98US-0103679P.  
PR 08-OCT-1998; 98US-0103711P.  
PR 14-OCT-1998; 98US-0104257P.  
PR 20-OCT-1998; 98US-0104987P.  
PR 20-OCT-1998; 98US-0105000P.  
PR 20-OCT-1998; 98US-0105002P.  
PR 21-OCT-1998; 98US-0105104P.  
PR 22-OCT-1998; 98US-0105169P.  
PR 22-OCT-1998; 98US-0105266P.  
PR 26-OCT-1998; 98US-0105693P.  
PR 26-OCT-1998; 98US-0105694P.  
PR 27-OCT-1998; 98US-0105807P.  
PR 27-OCT-1998; 98US-0105881P.  
PR 27-OCT-1998; 98US-0105882P.  
PR 27-OCT-1998; 98US-0106062P.  
PR 28-OCT-1998; 98US-0106023P.  
PR 28-OCT-1998; 98US-0106029P.  
PR 28-OCT-1998; 98US-0106030P.  
PR 28-OCT-1998; 98US-0106032P.  
PR 28-OCT-1998; 98US-0106033P.  
PR 28-OCT-1998; 98US-0106178P.  
PR 29-OCT-1998; 98US-0106248P.  
PR 29-OCT-1998; 98US-0106384P.  
PR 29-OCT-1998; 98US-0108500P.  
PR 30-OCT-1998; 98US-0106464P.

PR 03-NOV-1998; 98US-0106856P.  
PR 03-NOV-1998; 98US-0106902P.  
PR 03-NOV-1998; 98US-0106905P.  
PR 03-NOV-1998; 98US-0106919P.  
PR 03-NOV-1998; 98US-0106932P.  
PR 03-NOV-1998; 98US-0106934P.  
PR 10-NOV-1998; 98US-0107783P.  
PR 17-NOV-1998; 98US-0108775P.  
PR 17-NOV-1998; 98US-0108779P.  
PR 17-NOV-1998; 98US-0108787P.  
PR 17-NOV-1998; 98US-0108788P.  
PR 17-NOV-1998; 98US-0108801P.  
PR 17-NOV-1998; 98US-0108802P.  
PR 17-NOV-1998; 98US-0108806P.  
PR 17-NOV-1998; 98US-0108807P.  
PR 17-NOV-1998; 98US-0108867P.  
PR 17-NOV-1998; 98US-0108925P.  
PR 18-NOV-1998; 98US-0108848P.  
PR 18-NOV-1998; 98US-0108849P.  
PR 18-NOV-1998; 98US-0108850P.  
PR 18-NOV-1998; 98US-0108851P.  
PR 18-NOV-1998; 98US-0108852P.  
PR 18-NOV-1998; 98US-0108858P.  
PR 18-NOV-1998; 98US-0108904P.  
XX  
PA  
XX  
PI  
XX  
XX  
DR  
DR  
XX  
PT  
PT  
PT  
XX  
PS  
XX  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
XX  
SQ

(GETH ) GENENTECH INC.

Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;

WPI; 2000-237871/20.

P-PSDB; AAY99372.

New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions.

Claim 2; Fig 65; 773pp; English.

AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention

Sequence 1808 BP; 349 A; 545 C; 571 G; 343 T; 0 U; 0 Other;

Query Match 100.0%; Score 1808; DB 3; Length 1808;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1808; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTACCCAGGCGGCTGGTGTGTCAGCAAGCTCCGCGCGGACTCCGACGCGCTGACGCCT 60  
|||  
Db 1 GAGCTACCCAGGCGGCTGGTGTGTCAGCAAGCTCCGCGCGGACTCCGACGCGCTGACGCCT 60  
61 GACGCGCTGTCCCGGCGCGGCGCATGAGCCGCTACCTGTGCGGCTGTGCGGCGGCAAG 120  
61 GACGCGCTGTCCCGGCGCGGCGCATGAGCCGCTACCTGTGCGGCTGTGCGGCGGCAAG 120  
121 GTAGCAGGCGCGCGGCTGGTGTGTCAGCAAGCTATGTACCGGTGGGCTGCCCGCAGCAAG 180  
121 GTAGCAGGCGCGCGGCTGGTGTGTCAGCAAGCTATGTACCGGTGGGCTGCCCGCAGCAAG 180  
181 GCCACCATCCCTGGGAAGACGGTTCATCGTACGCGGCGGCGCAACACAGGATCGGGAAGCAG 240  
181 GCCACCATCCCTGGGAAGACGGTTCATCGTACGCGGCGGCGCAACACAGGATCGGGAAGCAG 240  
241 ACCGCGCTTGGAACTGGCCAGGAGAGGAGGAGCAACATCATCTGGCTGCCGAGACATGGAG 300  
241 ACCGCGCTTGGAACTGGCCAGGAGAGGAGGAGCAACATCATCTGGCTGCCGAGACATGGAG 300  
Db

QY 301 AAGTGTGAGCGGCGAGCAAAAGGACATCCGCGGGAGACCCCTCAATCACCATGTCAACGCC 360  
Db |||||  
QY 301 AAGTGTGAGCGGCGAGCAAAAGGACATCCGCGGGAGACCCCTCAATCACCATGTCAACGCC 360  
Db |||||  
QY 361 CGGCACCTGGACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAAAGATCATTTGAA 420  
Db |||||  
QY 361 CGGCACCTGGACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAAAGATCATTTGAA 420  
Db |||||  
QY 421 GAGGAGGAGCGAGTGGACATTTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCACTGG 480  
Db |||||  
QY 421 GAGGAGGAGCGAGTGGACATTTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCACTGG 480  
Db |||||  
QY 481 ACCACCGAGGACGGCTTCGAGATGCAGTTTGGCGTTAACCACTTGGGTCACTTTCTCTTG 540  
Db |||||  
QY 481 ACCACCGAGGACGGCTTCGAGATGCAGTTTGGCGTTAACCACTTGGGTCACTTTCTCTTG 540  
Db |||||  
QY 541 ACAAACTTGCTGTGGACAAAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCG 600  
Db |||||  
QY 541 ACAAACTTGCTGTGGACAAAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCG 600  
Db |||||  
QY 601 TCCCTGGCCCCATGTTGCTGGGCACATAGACTTTGACGACTTGAACCTGGGACGAGGAAG 660  
Db |||||  
QY 601 TCCCTGGCCCCATGTTGCTGGGCACATAGACTTTGACGACTTGAACCTGGGACGAGGAAG 660  
Db |||||  
QY 661 TATAACACCAAAAGCCCTACTGCCAGAGCAAGCTCGCCCATCGTCTCTTCAACCAAGGAG 720  
Db |||||  
QY 661 TATAACACCAAAAGCCCTACTGCCAGAGCAAGCTCGCCCATCGTCTCTTCAACCAAGGAG 720  
Db |||||  
QY 721 CTGAGCCCGCGGCTGCAAGGCTCTGGTGTGACTGTCAAGCCCTTGACCCCCGGCGTGGCC 780  
Db |||||  
QY 721 CTGAGCCCGCGGCTGCAAGGCTCTGGTGTGACTGTCAAGCCCTTGACCCCCGGCGTGGCC 780  
Db |||||  
QY 781 AGGACAGAGCTGGGCAGACACACGGGCATCCATGGCTCCACCTTCTCCAGACCACTC 840  
Db |||||  
QY 781 AGGACAGAGCTGGGCAGACACACGGGCATCCATGGCTCCACCTTCTCCAGACCACTC 840  
Db |||||  
QY 841 GGGCCCATCTTCTGGCTGCTGGTCAAGAGCCCCGAGCTGGCCCCAGCCCCAGCACATAC 900  
Db |||||  
QY 841 GGGCCCATCTTCTGGCTGCTGGTCAAGAGCCCCGAGCTGGCCCCAGCCCCAGCACATAC 900  
Db |||||  
QY 901 CTGGCGTGGCGGAGGAACCTGGCGGATGTTTCCGGAAAGTACTTCGATGGACTCAAAACAG 960  
Db |||||  
QY 901 CTGGCGTGGCGGAGGAACCTGGCGGATGTTTCCGGAAAGTACTTCGATGGACTCAAAACAG 960  
Db |||||  
QY 961 AAGGCCCGGCCCCCGAGGCTAGAGGCTCCCTCTGTGAGGGAGAGGCTTGGGCTGAAAGT 1020  
Db |||||  
QY 961 AAGGCCCGGCCCCCGAGGCTAGAGGCTCCCTCTGTGAGGGAGAGGCTTGGGCTGAAAGT 1020  
Db |||||  
QY 1021 GCGCGCTGTGGGCTTAGAGGCTCCCTCTGTGAGGGAGAGGCTTGGGCTGAAAGT 1080  
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QY 1021 GCGCGCTGTGGGCTTAGAGGCTCCCTCTGTGAGGGAGAGGCTTGGGCTGAAAGT 1080  
Db |||||  
QY 1081 CTGGAGCAGATTGAAAGCCAGGATGGCGCTCCAGACCGAGGACAGCTGTCCGCCATGC 1140  
Db |||||  
QY 1081 CTGGAGCAGATTGAAAGCCAGGATGGCGCTCCAGACCGAGGACAGCTGTCCGCCATGC 1140  
Db |||||  
QY 1141 CCGCAGCTTCTTGGCACTACCTGAGCCGGGAGACCCAGGACTGGCGGCCCATGCCGC 1200  
Db |||||  
QY 1141 CCGCAGCTTCTTGGCACTACCTGAGCCGGGAGACCCAGGACTGGCGGCCCATGCCGC 1200  
Db |||||  
QY 1201 AGTAGGTTCTAGGGGCGGTGCTGGCCGAGTGGACTGGCCCTGAGGCTGAGCACTGCC 1260  
Db |||||  
QY 1201 AGTAGGTTCTAGGGGCGGTGCTGGCCGAGTGGACTGGCCCTGAGGCTGAGCACTGCC 1260  
Db |||||  
QY 1261 GGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAGAGGGGCCATCTGATGCTT 1320  
Db |||||  
QY 1261 GGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAGAGGGGCCATCTGATGCTT 1320  
Db |||||  
QY 1321 CCCCTGGGAATCTAAACTGGGAATGGCCCGAGGAGGAAGGGGCTCTGTGCACTTGCAGGCC 1380  
Db |||||  
QY 1321 CCCCTGGGAATCTAAACTGGGAATGGCCCGAGGAGGAAGGGGCTCTGTGCACTTGCAGGCC 1380  
Db |||||

QY 1381 ACGTCAGGAGAGCCAGCGGTGCCTGTGCGGGAGGGTTCCAAGGTGCTCCGTGAAGAGCAT 1440  
Db |||||  
QY 1381 ACGTCAGGAGAGCCAGCGGTGCCTGTGCGGGAGGGTTCCAAGGTGCTCCGTGAAGAGCAT 1440  
Db |||||  
QY 1441 GGGCAAGTTGTCTGACACTTGGTGGATTCTTGGTCCCTGTGGACCTTGTGCATGCATG 1500  
Db |||||  
QY 1441 GGGCAAGTTGTCTGACACTTGGTGGATTCTTGGTCCCTGTGGACCTTGTGCATGCATG 1500  
Db |||||  
QY 1501 GTCTCTCTGAGCCCTTGGTTCTTTCAGCAGTGAGATGCTCAGAAATAACTGTCTCTCCCA 1560  
Db |||||  
QY 1501 GTCTCTCTGAGCCCTTGGTTCTTTCAGCAGTGAGATGCTCAGAAATAACTGTCTCTCCCA 1560  
Db |||||  
QY 1561 TGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGGTGTTG 1620  
Db |||||  
QY 1561 TGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGGTGTTG 1620  
Db |||||  
QY 1621 CTGAGGGCTTCCCTGTGCCAGAGCCCCAGCCAGAGAGCAGGTGCAGGTGTCAFCGCGAGTTC 1680  
Db |||||  
QY 1621 CTGAGGGCTTCCCTGTGCCAGAGCCCCAGCCAGAGAGCAGGTGCAGGTGTCAFCGCGAGTTC 1680  
Db |||||  
QY 1681 AGGCTCTGCACGGCATGGAGTGGAAACCCACCCAGCTGCTACAGGACCTGGGATTGC 1740  
Db |||||  
QY 1681 AGGCTCTGCACGGCATGGAGTGGAAACCCACCCAGCTGCTACAGGACCTGGGATTGC 1740  
Db |||||  
QY 1741 CTGGACTCCCACTTCCCTATCAATTCTCATGGTAGTCCAAACTGCAGACTCTCAAACTT 1800  
Db |||||  
QY 1741 CTGGACTCCCACTTCCCTATCAATTCTCATGGTAGTCCAAACTGCAGACTCTCAAACTT 1800  
Db |||||  
QY 1801 GCTCATTT 1808  
Db |||||  
QY 1801 GCTCATTT 1808  
Db |||||

RESULT 2

ID AAF54284 standard; DNA; 1808 BP.  
XX

AC AAF54284;

DT 02-APR-2001 (first entry)

DE DNA encoding protein of the invention #33.

KW Secreted; transmembrane; gene therapy; ss.

XX Unidentified.

PN WO200078961-A1;

XX 28-DEC-2000.

PF 18-FEB-2000; 2000WO-US004342.

XX 23-JUN-1999; 99US-0141037P.

PR 20-JUL-1999; 99US-0144758P.

PR 26-JUL-1999; 99US-0145698P.

PR 01-SEP-1999; 99WO-US020111.

PR 29-OCT-1999; 99US-0162506P.

PR 30-NOV-1999; 99WO-US028313.

PR 02-DEC-1999; 99WO-US028551.

PR 16-DEC-1999; 99WO-US030095.

PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000376.

XX (GETH ) GENENTECH INC.

XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;

PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;

PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;

PI Williams PM, Wood WI;

XX WPI; 2001-071395/08.

DR XX



PT Secreted and transmembrane proteins and nucleic acids designated PRO,  
PT useful as hybridization probes, in chromosome and gene mapping and gene  
PT therapy.

XX Claim 2; Fig 65; 787pp; English.

CC The present invention relates to secreted and transmembrane proteins.  
CC These proteins and the DNA encoding them may be used as hybridization  
CC probes, in chromosome and gene mapping and in the generation of anti-  
CC sense RNA and DNA. They may also be used to generate either  
CC transgenic animals or knockout animals which are in turn useful for  
CC development and screening of therapeutically useful reagents. The nucleic  
CC acids may also be used in gene therapy

XX  
SQ Sequence 1808 BP; 349 A; 545 C; 571 G; 343 T; 0 U; 0 Other;

Query Match 100.0%; Score 1808; DB 4; Length 1808;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1808; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GAGTACCCAGGCGGTGTGTGCAGCAAGCTCCGCGCGACTCCGACGCTGACGCT	60
Db	1	GAGTACCCAGGCGGTGTGTGCAGCAAGCTCCGCGCGACTCCGACGCTGACGCT	60
QY	61	GACGCTGTCCCGCGCGCATGAGCCGCTACCTGTGCGCGTGTGCGCGTGGGACG	120
Db	61	GACGCTGTCCCGCGCGCATGAGCCGCTACCTGTGCGCGTGTGCGCGTGGGACG	120
QY	121	GTAGCAGGCGCGCGCTGTCTCAAGGACTATGTACCCGTTGGGCTTCCCCCAGCAAG	180
Db	121	GTAGCAGGCGCGCGCTGTCTCAAGGACTATGTACCCGTTGGGCTTCCCCCAGCAAG	180
QY	181	GCCACCATCCCTGGGAAGACGGTCTATCGTGACGGGCGCCCAACACAGGATCGGGAAGCAG	240
Db	181	GCCACCATCCCTGGGAAGACGGTCTATCGTGACGGGCGCCCAACACAGGATCGGGAAGCAG	240
QY	241	ACCGCTTGGAACTGGCCAGGAGAGGAGGCAACATCATCTGGCCTGCCGAGACATGGAG	300
Db	241	ACCGCTTGGAACTGGCCAGGAGAGGAGGCAACATCATCTGGCCTGCCGAGACATGGAG	300
QY	301	AAGTGTAGGCGGCGAGCAAGAGACATCCGCGGGAGACCCCTCAATCACCATGTCAACGCC	360
Db	301	AAGTGTAGGCGGCGAGCAAGAGACATCCGCGGGAGACCCCTCAATCACCATGTCAACGCC	360
QY	361	CGGACCTGGACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAGATCATTTGAA	420
Db	361	CGGACCTGGACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAGATCATTTGAA	420
QY	421	GAGGAGGAGCGAGTGGACATTTCTAATCAACACCGCGGTGTGATCGGTTGCCCACTGG	480
Db	421	GAGGAGGAGCGAGTGGACATTTCTAATCAACACCGCGGTGTGATCGGTTGCCCACTGG	480
QY	481	ACCACGAGGACGGCTTCGAGATGCAAGTTTGGCGTTAACACCTGGGTCACTTCTCTTG	540
Db	481	ACCACGAGGACGGCTTCGAGATGCAAGTTTGGCGTTAACACCTGGGTCACTTCTCTTG	540
QY	541	ACAACTTGTCTGGAACAAGCTGAAGCCCTCAGCCCTTCGCGGATCATCAACCTCTCG	600
Db	541	ACAACTTGTCTGGAACAAGCTGAAGCCCTCAGCCCTTCGCGGATCATCAACCTCTCG	600
QY	601	TCCCTGGCCCATGTTGCTGGGCATAGACTTTGACACTTGAAGCTGGCAGACGAGGAAG	660
Db	601	TCCCTGGCCCATGTTGCTGGGCATAGACTTTGACACTTGAAGCTGGCAGACGAGGAAG	660
QY	661	TATAACACCAAGCCGCTACTGCCAGAGCAAGCTCGCCATCGTCTCTTACCAAGGAG	720
Db	661	TATAACACCAAGCCGCTACTGCCAGAGCAAGCTCGCCATCGTCTCTTACCAAGGAG	720
QY	721	CTGAGCCGGCGCTGCAAGGCTCTGGTGTGACTGTGCCATCGTCTCTTACCAAGGAG	780
Db	721	CTGAGCCGGCGCTGCAAGGCTCTGGTGTGACTGTGCCATCGTCTCTTACCAAGGAG	780
QY	781	AGGACAGAGCTGGGCGAGACACACGGGCGATCCATGGCTCCACCTTCTCCAGCACCACTC	840

Db	781	AGGACAGAGCTGGGCGAGACACACGGGCGATCCATGGCTCCACCTTCTCCAGCACCACTC	840
QY	841	GGGCCCCATCTTCTGGTGTGCTGCTCAAGAGCCCGAGCTGGCGCCAGCCAGCACATAC	900
Db	841	GGGCCCCATCTTCTGGTGTGCTGCTCAAGAGCCCGAGCTGGCGCCAGCCAGCACATAC	900
QY	901	CTGGCCGTGGCGGAGAACTGGCGGATGTTTCCGGAAGTACTTCGATGGACTCAAACAG	960
Db	901	CTGGCCGTGGCGGAGAACTGGCGGATGTTTCCGGAAGTACTTCGATGGACTCAAACAG	960
QY	961	AAGGCCCCGCGCCCGAGGCTGAGGATGAGGAGGTGGCCCGGAGGCTTTGGGCTGAAAGT	1020
Db	961	AAGGCCCCGCGCCCGAGGCTGAGGATGAGGAGGTGGCCCGGAGGCTTTGGGCTGAAAGT	1020
QY	1021	GCCCGCTGGTGGGCTTAGAGGCTCCCTCTGTGAGGAGCAGCCCTCCAGATAACCT	1080
Db	1021	GCCCGCTGGTGGGCTTAGAGGCTCCCTCTGTGAGGAGCAGCCCTCCAGATAACCT	1080
QY	1081	CTGGAGCAGATTGAAAGCCAGGATGGCGCTCCAGACCGAGGACAGCTGTCCGCCATGC	1140
Db	1081	CTGGAGCAGATTGAAAGCCAGGATGGCGCTCCAGACCGAGGACAGCTGTCCGCCATGC	1140
QY	1141	CCGACGCTTCTGGCACTACCTGAGCCGGAGACCCAGGACTGGCGCCGCTGCCCCG	1200
Db	1141	CCGACGCTTCTGGCACTACCTGAGCCGGAGACCCAGGACTGGCGCCGCTGCCCCG	1200
QY	1201	AGTAGGTTCTAGGGGCGGTGCTGGCCGAGTGGACTGGCCTGAGGTGAGCACTGCCCC	1260
Db	1201	AGTAGGTTCTAGGGGCGGTGCTGGCCGAGTGGACTGGCCTGAGGTGAGCACTGCCCC	1260
QY	1261	GGGCTCTGGTGGTTCGCTCTGCTGCTGCGCAGCAGGGGAGAGGGGCGCATCTGATGCTT	1320
Db	1261	GGGCTCTGGTGGTTCGCTCTGCTGCTGCGCAGCAGGGGAGAGGGGCGCATCTGATGCTT	1320
QY	1321	CCCCTGGGAATCTAAACTGGGAATGGCCGAGAGGAGGAGGCTCTGTGCACTTGCAGGCC	1380
Db	1321	CCCCTGGGAATCTAAACTGGGAATGGCCGAGAGGAGGAGGCTCTGTGCACTTGCAGGCC	1380
QY	1381	ACGTAGGAGAGCCAGCGGTGCTGTCGCGGAGGGTTTCCAAAGTGTCCGTGAAGAGCAT	1440
Db	1381	ACGTAGGAGAGCCAGCGGTGCTGTCGCGGAGGGTTTCCAAAGTGTCCGTGAAGAGCAT	1440
QY	1441	GGCAAGTTGTCTGACACTTGGTGGATTCTTGGTCCCTGTGGGACCTTGTGCATGTCATG	1500
Db	1441	GGCAAGTTGTCTGACACTTGGTGGATTCTTGGTCCCTGTGGGACCTTGTGCATGTCATG	1500
QY	1501	GTCTCTCTGAGCCCTTGGTTTCTTCAGCAGTGAATGCTCAGATAACTGTGTCTCCCA	1560
Db	1501	GTCTCTCTGAGCCCTTGGTTTCTTCAGCAGTGAATGCTCAGATAACTGTGTCTCCCA	1560
QY	1561	TGATGTTGTGTACAGCAGCTGTTGTCTGGCTATGGCATGGCTGTCCCGGGGTGTTG	1620
Db	1561	TGATGTTGTGTACAGCAGCTGTTGTCTGGCTATGGCATGGCTGTCCCGGGGTGTTG	1620
QY	1621	CTGAGGCTTCTGTGTCAGAGCCCGAGAGAGCAGGTCAGGTCATCCCGAGTTC	1680
Db	1621	CTGAGGCTTCTGTGTCAGAGCCCGAGAGAGCAGGTCAGGTCATCCCGAGTTC	1680
QY	1681	AGGCTCTGACGGCATGGAGTGGGAACCCCACTGCTGTCTACAGGACCTGGGATTGC	1740
Db	1681	AGGCTCTGACGGCATGGAGTGGGAACCCCACTGCTGTCTACAGGACCTGGGATTGC	1740
QY	1741	CTGGAGTCCCACTTCTTCTATCAATTTCTCATGGTAGTCCAAACTGCAGACTCTCAAACTT	1800
Db	1741	CTGGAGTCCCACTTCTTCTATCAATTTCTCATGGTAGTCCAAACTGCAGACTCTCAAACTT	1800
QY	1801	GCTCATTT 1808	
Db	1801	GCTCATTT 1808	

RESULT 3

[illegible]



PR	18-NOV-1998;	98US-0108850P.	
PR	18-NOV-1998;	98US-0108851P.	
PR	18-NOV-1998;	98US-0108852P.	
PR	18-NOV-1998;	98US-0108858P.	
PR	18-NOV-1998;	98US-0108904P.	
PR	22-DEC-1998;	98US-0113296P.	
PR	30-DEC-1998;	98US-0114223P.	
PR	05-JAN-1999;	99WO-US000106.	
PR	16-APR-1999;	99US-0129674P.	
PR	23-JUN-1999;	99US-0141037P.	
PR	20-JUL-1999;	99US-0144758P.	
PR	26-JUL-1999;	99US-0145698P.	
PR	01-SEP-1999;	99WO-US020111.	
PR	15-SEP-1999;	99WO-US021194.	
PR	29-OCT-1999;	99US-0162506P.	
PR	30-NOV-1999;	99WO-US028313.	
PR	02-DEC-1999;	99WO-US028551.	
PR	16-DEC-1999;	99WO-US030095.	
PR	05-JAN-2000;	2000WO-US000219.	
PR	06-JAN-2000;	2000WO-US000376.	
PR	11-FEB-2000;	2000WO-US0003565.	
PR	18-FEB-2000;	2000WO-US004342.	
PR	24-FEB-2000;	2000WO-US005004.	
PR	02-MAR-2000;	2000WO-US005841.	
PR	15-MAR-2000;	2000WO-US006884.	
PR	17-MAY-2000;	2000WO-US013705.	
PR	22-MAY-2000;	2000WO-US014042.	
PR	30-MAY-2000;	2000WO-US014941.	
PR	02-JUN-2000;	2000WO-US015264.	
PR	23-AUG-2000;	2000WO-US023522.	
PR	24-AUG-2000;	2000WO-US023328.	
PR	08-NOV-2000;	2000WO-US030952.	
PR	10-NOV-2000;	2000WO-US030873.	
PR	01-DEC-2000;	2000WO-US032678.	
PR	28-FEB-2001;	2001WO-US006520.	
PR	01-MAR-2001;	2001WO-US006666.	
PR	01-JUN-2001;	2001WO-US017800.	
PR	20-JUN-2001;	2001WO-US019692.	
PR	29-JUN-2001;	2001WO-US021066.	
PR	09-JUL-2001;	2001WO-US021735.	
PR	04-SEP-2001;	2001US-00946374.	
XX			
PA	(GETH ) GENENTECH INC.		
XX			
PI	Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;		
PI	Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;		
PI	Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CX;		
PI	Williams PM, Wood WI;		
XX			
DR	WPI; 2003-585293/55.		
DR	P-PSDB; ABO33614.		
XX			
PT	Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,		
PT	PRO1787 that modulate glucose or free fatty acid uptake by skeletal		
PT	muscle cells, and are useful for treating diabetes, hyper- or hypo-		
	Query Match 100.0%; Score 1808; DB 8; Length 1808;		
	Best Local Similarity 100.0%; Pred. No. 0;		
	Matches 1808; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 GAGCTACCCAGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCCTGACGCCT 60		
Db	1 GAGCTACCCAGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCCTGACGCCT 60		
QY	61 GACGCCTGTCCCGGCCCGGCATGAGCCGCTACCTGTGCCGTGTTCGGCGCTGGGCACG 120		
Db	61 GACGCCTGTCCCGGCCCGGCATGAGCCGCTACCTGTGCCGTGTTCGGCGCTGGGCACG 120		
QY	121 GTAGCAGGCGCGCGTGTCTCAAGACTATGTCAACCGTGGGGCTTGCCCCAGCAAG 180		
Db	121 GTAGCAGGCGCGCGTGTCTCAAGACTATGTCAACCGTGGGGCTTGCCCCAGCAAG 180		
QY	181 GCCACCATCCCTGGGAAGACGGTCACTCGTAGCGGGGCCCAACACAGGCATCGGGAAGCAG 240		

Db	181 GCCACCATCCCTGGGAAGACGGTCACTCGTAGCGGGGCCCAACACAGGCATCGGGAAGCAG 240	
QY	241 ACCGCTTTGGAACCTGGCCAGGAGAGGAGGCAACATCATCTGGCTTCCGAGACATGGAG 300	
Db	241 ACCGCTTTGGAACCTGGCCAGGAGAGGAGGCAACATCATCTGGCTTCCGAGACATGGAG 300	
QY	301 AAGTGTGAGCGGCGAGCAAAAGACATCCGCGGGAGACCCCTCAATCACCATGTCAACGCC 360	
Db	301 AAGTGTGAGCGGCGAGCAAAAGACATCCGCGGGAGACCCCTCAATCACCATGTCAACGCC 360	
QY	361 CGGCACCTGGACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAAAGATCATTTGAA 420	
Db	361 CGGCACCTGGACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAAAGATCATTTGAA 420	
QY	421 GAGGAGGAGCGAGTGGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCACTGG 480	
Db	421 GAGGAGGAGCGAGTGGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCACTGG 480	
QY	481 ACCACCGAGGACGGCTTCGAGATGCAGTTTGGCGTTAACACACCTGGGTCACTTTCTTTG 540	
Db	481 ACCACCGAGGACGGCTTCGAGATGCAGTTTGGCGTTAACACACCTGGGTCACTTTCTTTG 540	
QY	541 ACAAACCTTGTCTGTGGACAAAGCTGAAAGCCTCAGCCCTTCGCGGATCATCAACCTCTCG 600	
Db	541 ACAAACCTTGTCTGTGGACAAAGCTGAAAGCCTCAGCCCTTCGCGGATCATCAACCTCTCG 600	
QY	601 TCCCTGGCCCCATGTTGCTGGSCACATAGACTTTTGACGACTTGAACCTGGCAGAGGAAG 660	
Db	601 TCCCTGGCCCCATGTTGCTGGSCACATAGACTTTTGACGACTTGAACCTGGCAGAGGAAG 660	
QY	661 TATAACACCAAGCGCCTACTCCAGAGCAAGCTCGCCCTCTTCCACCAAGGAG 720	
Db	661 TATAACACCAAGCGCCTACTCCAGAGCAAGCTCGCCCTCTTCCACCAAGGAG 720	
QY	721 CTGAGCGCGGCTGCAAGGCTCTGGTGTGACTGTCAACGCCCTGCACCCCGCGTGGCC 780	
Db	721 CTGAGCGCGGCTGCAAGGCTCTGGTGTGACTGTCAACGCCCTGCACCCCGCGTGGCC 780	
QY	781 AGGACAGAGCTGGCAGACACACGGGCATCCATGGCTCCACCTTCTCCAGCACCACTC 840	
Db	781 AGGACAGAGCTGGCAGACACACGGGCATCCATGGCTCCACCTTCTCCAGCACCACTC 840	
QY	841 GGGCCCATCTTCTGGCTGTGTGTCAAGAGCCCCGAGCTGGCCCGCCAGCCAGCACATAC 900	
Db	841 GGGCCCATCTTCTGGCTGTGTGTCAAGAGCCCCGAGCTGGCCCGCCAGCCAGCACATAC 900	
QY	901 CTGGCCGTGGCGGAGGAACCTGGCGGATGTTTCCGGAAGTACTTTCGATGGACTCAACAG 960	
Db	901 CTGGCCGTGGCGGAGGAACCTGGCGGATGTTTCCGGAAGTACTTTCGATGGACTCAACAG 960	
QY	961 AAGGCCCGGCCCGGCTGAGGCTGAGGAGTGGCCCGGAGGCTTTGGGCTGAAAGT 1020	
Db	961 AAGGCCCGGCCCGGCTGAGGCTGAGGAGTGGCCCGGAGGCTTTGGGCTGAAAGT 1020	
QY	1021 GCCCGCTGGTGGGCTTAGAGGCTCCCTCTGTGAGGGAGCAGCCCTTCCCGAGATAACCT 1080	
Db	1021 GCCCGCTGGTGGGCTTAGAGGCTCCCTCTGTGAGGGAGCAGCCCTTCCCGAGATAACCT 1080	
QY	1081 CTGGAGCAGATTGAAAGCCAGGATGGCGCCTCCAGACCGAGGACAGCTGTCCGCCATGC 1140	
Db	1081 CTGGAGCAGATTGAAAGCCAGGATGGCGCCTCCAGACCGAGGACAGCTGTCCGCCATGC 1140	
QY	1141 CCGCAGCTTCTGGCACTACCTGAGCCGGGAGACCCAGGACTGGCGCCCGCATGCCCGC 1200	
Db	1141 CCGCAGCTTCTGGCACTACCTGAGCCGGGAGACCCAGGACTGGCGCCCGCATGCCCGC 1200	
QY	1201 AGTAGGTTCTAGGGGGCGGTGCTGGCCCGCAGTGGACTGGCCCTGCAGGTGAGCACTGCC 1260	
Db	1201 AGTAGGTTCTAGGGGGCGGTGCTGGCCCGCAGTGGACTGGCCCTGCAGGTGAGCACTGCC 1260	
QY	1261 GGGCTCTGGTGGTTCCGTCTGCTGCTGCCAGAGGGGAGAGGGGCCATCTGATGCTT 1320	



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PR 21-OCT-1998; 98US-0105104P.  
PR 22-OCT-1998; 98US-0105169P.  
PR 22-OCT-1998; 98US-0105266P.  
PR 26-OCT-1998; 98US-0105693P.  
PR 26-OCT-1998; 98US-0105694P.  
PR 27-OCT-1998; 98US-0105807P.  
PR 27-OCT-1998; 98US-0105881P.  
PR 27-OCT-1998; 98US-0105882P.  
PR 27-OCT-1998; 98US-0106062P.  
PR 28-OCT-1998; 98US-0106023P.  
PR 28-OCT-1998; 98US-0106029P.  
PR 28-OCT-1998; 98US-0106030P.  
PR 28-OCT-1998; 98US-0106032P.  
PR 28-OCT-1998; 98US-0106033P.  
PR 28-OCT-1998; 98US-0106178P.  
PR 29-OCT-1998; 98US-0106248P.  
PR 29-OCT-1998; 98US-0106384P.  
PR 29-OCT-1998; 98US-0108500P.  
PR 30-OCT-1998; 98US-0106464P.  
PR 03-NOV-1998; 98US-0106856P.  
PR 03-NOV-1998; 98US-0106902P.  
PR 03-NOV-1998; 98US-0106905P.  
PR 03-NOV-1998; 98US-0106919P.  
PR 03-NOV-1998; 98US-0106932P.  
PR 03-NOV-1998; 98US-0106934P.  
PR 10-NOV-1998; 98US-0107783P.  
PR 17-NOV-1998; 98US-0108775P.  
PR 17-NOV-1998; 98US-0108779P.  
PR 17-NOV-1998; 98US-0108787P.  
PR 17-NOV-1998; 98US-0108788P.  
PR 17-NOV-1998; 98US-0108801P.  
PR 17-NOV-1998; 98US-0108802P.  
PR 17-NOV-1998; 98US-0108806P.  
PR 17-NOV-1998; 98US-0108807P.  
PR 17-NOV-1998; 98US-0108867P.  
PR 17-NOV-1998; 98US-0108925P.  
PR 18-NOV-1998; 98US-0108848P.  
PR 18-NOV-1998; 98US-0108849P.  
PR 18-NOV-1998; 98US-0108850P.  
PR 18-NOV-1998; 98US-0108851P.  
PR 18-NOV-1998; 98US-0108852P.  
PR 18-NOV-1998; 98US-0108858P.  
PR 18-NOV-1998; 98US-0108904P.  
PR 22-DEC-1998; 98US-0113296P.  
PR 30-DEC-1998; 98US-0114223P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 16-APR-1999; 99US-0129674P.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 15-SEP-1999; 99WO-US021194.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.

PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006566.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;  
XX  
DR WPI; 2003-492259/46.  
DR P-PSDB; ABO44467.  
XX  
PT Novel secreted and transmembrane polypeptides and polynucleotides  
PT encoding them useful for treating various cardiac insufficiency  
PT disorders, bone and/or cartilage disorders such as sports injuries and  
PT arthritis.  
  
Query Match 100.0%; Score 1808; DB 8; Length 1808;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1808; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GAGCTACCCAGCGGCTGGTGTGCAGCAAGCTCCGCGCGGACTCCGGACGCTGACGCCT 60  
|||  
Db 1 GAGCTACCCAGCGGCTGGTGTGCAGCAAGCTCCGCGCGGACTCCGGACGCTGACGCCT 60  
  
QY 61 GAGCCTGTCCCCGGCCGCGCATGAGCCGCTACCTGCTGCCGCTGTGCGGCGTGGGCACG 120  
|||  
Db 61 GAGCCTGTCCCCGGCCGCGCATGAGCCGCTACCTGCTGCCGCTGTGCGGCGTGGGCACG 120  
  
QY 121 GTAGCAGCGCGCCGCTGCTGCTCAAGGACTATGTACCGGTGGGGCTTGCCCCAGCAAG 180  
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QY 181 GCCACCATCCCTGGGAAGACGGTCACTGTGACGGGGGCCAACACAGGCATCGGGAAGCAG 240  
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Db 181 GCCACCATCCCTGGGAAGACGGTCACTGTGACGGGGGCCAACACAGGCATCGGGAAGCAG 240  
  
QY 241 ACCGCTTGGAACTGGCCAGGAGGAGGCAACATCATCTGGCCTGCCGAGACATGGAG 300  
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Db 241 ACCGCTTGGAACTGGCCAGGAGGAGGCAACATCATCTGGCCTGCCGAGACATGGAG 300  
  
QY 301 AAGTGTAGCGCGGAGCAAAAGGACATCCGCGGGGAGACCTCAATCACCATGTCAACGCC 360  
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Db 301 AAGTGTAGCGCGGAGCAAAAGGACATCCGCGGGGAGACCTCAATCACCATGTCAACGCC 360  
  
QY 361 CGGCACCTGGACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAAAGATCATTGAA 420  
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Db 361 CGGCACCTGGACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAAAGATCATTGAA 420  
  
QY 421 GAGGAGGAGCGAGTGGACATTCTAATCAACAACCGGGTGTGATGCGGTGCCCCACTGG 480  
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Db 421 GAGGAGGAGCGAGTGGACATTCTAATCAACAACCGGGTGTGATGCGGTGCCCCACTGG 480  
  
QY 481 ACCACCGAGGACGGCTTCGAGATGCAAGTTTGGCGTTAACCACTGGGTCACTTTCTTTG 540  
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Db 481 ACCACCGAGGACGGCTTCGAGATGCAAGTTTGGCGTTAACCACTGGGTCACTTTCTTTG 540  
  
QY 541 ACAAACTTGCTGTGGACAAGCTGAAAAGCCTCAGCCCTTCGCGGATCATCAACCTCTCG 600  
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Db 541 ACAAACTTGCTGTGGACAAGCTGAAAAGCCTCAGCCCTTCGCGGATCATCAACCTCTCG 600  
  
QY 601 TCCCTGGCCCATGTTGCTGGGCACATAGACTTTTGACGACTTGAACCTGGCAGACGAGGAAG 660  
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Db 601 TCCCTGGCCCATGTTGCTGGGCACATAGACTTTTGACGACTTGAACCTGGCAGACGAGGAAG 660  
  
QY 661 TATAACACCAAAAGCCGCTACTGCCAGAGCAAGCTCGCCATCGTCTCTTTCACCAAGGAG 720  
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Db 661 TATAACACCAAGCCGCTACTGCCAGAGCAAGCTGCCCATCGTCTCTTACCAAGGAG 720

Qy 721 CTGAGCCGGCGGCTGCAAGGCTCTGGTGTGACTGTCAACGCCCTGCACCCCGCGTGGCC 780

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Qy 781 AGGACAGAGCTGGGCAGACACACGGGCATCCATGGTCCACCTTCTCCAGACCACACTC 840

Db 781 AGGACAGAGCTGGGCAGACACACGGGCATCCATGGTCCACCTTCTCCAGACCACACTC 840

Qy 841 GGGCCCATCTTCTGGCTGCTGGTCAAGAGCCCCGAGTGGCCGCCAGCCAGCACATAC 900

Db 841 GGGCCCATCTTCTGGCTGCTGGTCAAGAGCCCCGAGTGGCCGCCAGCCAGCACATAC 900

Qy 901 CTGGCCGTGGCGAGGAACCTGGCGGATGTTTCCGGAAAGTACTTCGATGGACTCAAACAG 960

Db 901 CTGGCCGTGGCGAGGAACCTGGCGGATGTTTCCGGAAAGTACTTCGATGGACTCAAACAG 960

Qy 961 AAGGCCCGGCCCCGAGGCTGAGGATGAGGAGGTGGCCCCGAGGCTTTGGGCTGAAAGT 1020

Db 961 AAGGCCCGGCCCCGAGGCTGAGGATGAGGAGGTGGCCCCGAGGCTTTGGGCTGAAAGT 1020

Qy 1021 GCCCGCTGGTGGGCTTAGAGCTCCCTCTGTGAGGAGCAGCCCCCTCCCAGATAACCT 1080

Db 1021 GCCCGCTGGTGGGCTTAGAGCTCCCTCTGTGAGGAGCAGCCCCCTCCCAGATAACCT 1080

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Db 1081 CTGAGCAGATTTGAAAGCCAGATGGCGCTCCAGACCGAGGACAGCTGTCCGCCATGC 1140

Qy 1141 CCGAGACTTCTGGCACTACCTGAGCCGGGAGACCCAGACTGGCGGCCCATGCCCGC 1200

Db 1141 CCGAGACTTCTGGCACTACCTGAGCCGGGAGACCCAGACTGGCGGCCCATGCCCGC 1200

Qy 1201 AGTAGGTTCTAGGGGCGGTGCTGGCCGCGAGTGGACTGGCTGCGCTGAGCACTGCCCC 1260

Db 1201 AGTAGGTTCTAGGGGCGGTGCTGGCCGCGAGTGGACTGGCTGCGCTGAGCACTGCCCC 1260

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Db 1261 GGGCTCTGGCTGGTCCGTTCTGCTGTGCCAGCAGGGGAGAGGGCCATCTGATGCTT 1320

Qy 1321 CCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTCTGTGCATTCGAGGCC 1380

Db 1321 CCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTCTGTGCATTCGAGGCC 1380

Qy 1381 ACGTCAGAGAGCCAGCGGTGCTGTCGGGAGGTTCCAAAGGTGCTCCGTGAAGAGCAT 1440

Db 1381 ACGTCAGAGAGCCAGCGGTGCTGTCGGGAGGTTCCAAAGGTGCTCCGTGAAGAGCAT 1440

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Qy 1501 GTCCTCTTGAGCCTTGGTTTCTTCAGCAGTGAGATGCTCAGAATAACTGCTGTCTCCCA 1560

Db 1501 GTCCTCTTGAGCCTTGGTTTCTTCAGCAGTGAGATGCTCAGAATAACTGCTGTCTCCCA 1560

Qy 1561 TGATGGTGGTACAGCGAGCTGTTTCTTCAGCAGTGAGATGCTCAGAATAACTGCTGTCT 1620

Db 1561 TGATGGTGGTACAGCGAGCTGTTTCTTCAGCAGTGAGATGCTCAGAATAACTGCTGTCT 1620

Qy 1621 CTGAGGGGCTTCTGTGCCAGAGCCAGCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680

Db 1621 CTGAGGGGCTTCTGTGCCAGAGCCAGCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680

Qy 1681 AGGCTCTGACGGCATGGAGTGGGAACCCCAACCACTGCTGTCTACAGGACCTGGGATTGC 1740

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Db 1741 CTGGGACTCCCACTTCTTCTATCAATTTCTATGGTAGTCCAAACTGCAGACTCTCAAACCTT 1800

Qy 1801 GCTCATTT 1808

Db 1801 GCTCATTT 1808

RESULT 5

ACD67967

ID ACD67967 standard; cDNA; 1808 BP.

XX

AC ACD67967;

XX

DT 17-SEP-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO1430 cDNA.

XX

KW Human; secreted and transmembrane protein; PRO; gene therapy; vaccine;

KW tissue typing; chromosome identification; vaccine; gene; ss.

XX

OS Homo sapiens.

XX

PN US2003073129-A1.

XX

PD 17-APR-2003.

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PF 04-SEP-2001; 2001US-00946374.

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01-SEP-1998; 98US-0098716P.

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Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
Williams PM, Wood WI;

WPI; 2003-585292/55.  
P-PSDB; ABO33491.

Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the  
preparation of a medicament for treating a condition responsive to PRO  
polypeptide, and as therapeutic agents e.g. vaccines.

Claim 2; Fig 65; 561pp; English.

The invention describes an isolated PRO (secreted and transmembrane)  
polypeptide (I), having at least 80% sequence identity to a sequence

Query Match 100.0%; Score 1808; DB 8; Length 1808;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1808; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTACCCAGCGCGTGGTGTGCGAGCAAGCTCCGCCGACTCCGGACGCCTGACGCCT 60  
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Db 1 GAGCTACCCAGCGCGTGGTGTGCGAGCAAGCTCCGCCGACTCCGGACGCCTGACGCCT 60  
|||||

QY 61 GACGCCTGTCCCGCCCGGCGATGAGCCGCTACCTGTCCGCTGTCCGCGCTGGGCACG 120  
|||||



Db 61 GACGCCTGTCCCCGGCCCGGCATGAGCCGCTACTGTGCTGCCGTGTCCGGCTGGGCACG 120

Qy 121 GTAGCAGGCGCGCGCTGTGCTCAAGGACTATGTCAACGGTGGGCTTGCCCCAGCAAG 180

Db 121 GTAGCAGGCGCGCGCTGTGCTCAAGGACTATGTCAACGGTGGGCTTGCCCCAGCAAG 180

Qy 181 GCCACCATCCCTGGGAACACGGTCACTCGTGACGGGCGCCAAACACAGGCATCGGGAAGCAG 240

Db 181 GCCACCATCCCTGGGAACACGGTCACTCGTGACGGGCGCCAAACACAGGCATCGGGAAGCAG 240

Qy 241 ACCGCCCTTGGAACCTGGCCAGGAGAGGAGGCAACATCATCCTTGCCCTGCCGAGACATGGAG 300

Db 241 ACCGCCCTTGGAACCTGGCCAGGAGAGGAGGCAACATCATCCTTGCCCTGCCGAGACATGGAG 300

Qy 301 AAGTGTAGCGCGCAGCAAAAGACATCCGCGGGAGACCTCAATCAACATGTCAACGCC 360

Db 301 AAGTGTAGCGCGCAGCAAAAGACATCCGCGGGAGACCTCAATCAACATGTCAACGCC 360

Qy 361 CGGCACCTGGACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGACGAAAAGATCATTTGAA 420

Db 361 CGGCACCTGGACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGACGAAAAGATCATTTGAA 420

Qy 421 GAGGAGGACGAGTGGACATTCTAATCAACAACGCGGGTGTGATCGGTCGCCCCACTGG 480

Db 421 GAGGAGGACGAGTGGACATTCTAATCAACAACGCGGGTGTGATCGGTCGCCCCACTGG 480

Qy 481 ACCACCGAGGACGGCTTCGAGATGCAGTTTGGCGTTAACCCACTGGGTCACTTTCTCTTG 540

Db 481 ACCACCGAGGACGGCTTCGAGATGCAGTTTGGCGTTAACCCACTGGGTCACTTTCTCTTG 540

Qy 541 ACAAACCTTGCTGTGACAAAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCG 600

Db 541 ACAAACCTTGCTGTGACAAAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCG 600

Qy 601 TCCCTGGCCCCATGTTGTGGGCACATAGACTTTGACGACTTTGAACTGGCAGACGAGGAAG 660

Db 601 TCCCTGGCCCCATGTTGTGGGCACATAGACTTTGACGACTTTGAACTGGCAGACGAGGAAG 660

Qy 661 TATAACACCAAAGCCCGCTACTGCCAGAGCAAGCTGCCCATCGTCCCTTTTCAACCAAGGAG 720

Db 661 TATAACACCAAAGCCCGCTACTGCCAGAGCAAGCTGCCCATCGTCCCTTTTCAACCAAGGAG 720

Qy 721 CTGAGCCGGCGGCTGCAAGGCTCTGGTGTGACTGTCAACGCCCTGCACCCCGCGTGGCC 780

Db 721 CTGAGCCGGCGGCTGCAAGGCTCTGGTGTGACTGTCAACGCCCTGCACCCCGCGTGGCC 780

Qy 781 AGGACAGAGCTGGGCAGACACACGGGCATCCATGGCTCCACCTTCTCAGCACCAACATC 840

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Qy 841 GGGCCCCATCTTCTGGCTGTGGTCAAGAGCCCCGAGCTGGCCGCCAGCCAGCACATAC 900

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Qy 901 CTGGCCGTGGCGAGGAACTGGCGGATGTTTCCGGAAGTACTTCGATGGACTCAAACAG 960

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Qy 961 AAGGCCCCGGCCCCGAGGCTGAGGATGAGGAGTGGCCCGGAGGCTTGGGCTGAAAGT 1020

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Qy 1021 GCCCGCTGGTGGCTTAGAGGCTCCCTCTGTGAGGAGCAGCCCTCCCGAGATAACCT 1080

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Qy 1081 CTGGAGCAGATTTGAAAGCCAGGATGGCGCTCCAGACCGAGGACAGCTGTCGCCATGC 1140

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Db 1141 CCGCAGCTTCTCTGGCACACTACTGAGCCGGGAGACCCAGGACTGGCGGCCCATGCCCGC 1200

Qy 1201 AGTAGGTTCTAGSGGSCGTGCTGGCCGCAGTGGACTGGCCTGCAGGTGAGCACTGCCCC 1260

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Db 1321 CCCCTGGGAATCTAAACTGGGAATGGCCCGAGAGGAAGGGGCTCTGTGCACTTTGCAGGCC 1380

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Qy 1501 GTCCTCTCTGAGCCCTGGTTTCTTCAGCAGTGAGATGCTCAGAAATACTGCTCTCCTCA 1560

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Qy 1801 GCTCATTT 1808

Db 1801 GCTCATTT 1808

RESULT 6

ADC17984

ID ADC17984 standard; cDNA; 1808 BP.

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AC ADC17984;

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DT 18-DEC-2003 (first entry)

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DE Human PRO polynucleotide #33.

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KW Human; PRO; gene; ss; protein electrophoresis; chromosome mapping;

KW gene mapping; genetic disorder.

OS Homo sapiens.

XX

XX US2003064925-A1.

PN

XX

PD 03-APR-2003.

XX

PF 10-DEC-2001; 2001US-00013907.

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PR 18-NOV-1998; 98US-0108849P.  
PR 18-NOV-1998; 98US-0108850P.  
PR 18-NOV-1998; 98US-0108851P.  
PR 18-NOV-1998; 98US-0108852P.  
PR 18-NOV-1998; 98US-0108858P.  
PR 18-NOV-1998; 98US-0108904P.  
PR 22-DEC-1998; 98US-0113296P.  
PR 30-DEC-1998; 98US-0114223P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 16-APR-1999; 99US-0129674P.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 15-SEP-1999; 99WO-US021194.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.

PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.  
XX  
PA (GETH ) GENENTECH INC.  
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams EM, Wood WI;  
XX  
DR WPI; 2003-555602/52.  
DR P-PSDB; ADCI17985.  
XX  
PT Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the  
PT preparation of a medicament for treating a condition responsive to PRO  
PT polypeptide, and as therapeutic agents e.g. vaccines.  
XX  
PS Claim 2; SEQ ID NO 115; 555pp; English.  
XX  
CC The invention relates to human PRO polypeptides and the polynucleotides  
CC encoding them. The sequences are useful in the preparation of a  
CC medicament for treating a condition responsive to a PRO polypeptide. The  
CC polypeptides are useful in a number of functional biological assays, as  
CC molecular weight markers for protein electrophoresis and as therapeutic

Query Match 100.0%; Score 1808; DB 9; Length 1808;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1808; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 GTAGAGGCGCGCGCTGTGCTCAAGGACTATGTACCGTGGGCTTGCCCCAGCAAG 180  
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QY 181 GCCACATCCCTGGGAAGACGGTCACTGTGACGGGCGCAACACAGGCATCGGGAAGCAG 240  
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QY 301 AAGTGTGAGCGGCAGCAAAAGGACATCCGGGGAGACCTCAATCACCATGTCAACGCC 360  
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QY 361 CGGCACCTGGACTTGGCTTCCCTCAAGTCTATCCGAGAGTTGACGAAAGATCATTTGAA 420  
Db |||||  
QY 421 GAGGAGGAGCGAGTGGACATTCATTAACAACACGCGGGGTGTGATCGGTCGCCCACTGG 480  
Db |||||  
QY 481 ACCACCGAGGACGGCTTCGAGATGCAGTTTGGCGTTAACACACCTGGGTCACTTCTTTG 540  
Db |||||  
QY 541 ACAAACTTGTCTGGACAAGCTGAAAGCCTCAGCCCCCTTGGCGGATCATCAACCTCTCG 600  
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QY 601 TCCCTGGCCCATGTTGCTGGGCACATAGACTTTTGACGACTTGAACTGGCAGACGAGGAAG 660  
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QY 721 CTGAGCCGCGGCTGCAAGGCTCTGGTGTGACTGTCAACGCCCTGCACCCCGGCTGGCC 780  
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QY 781 AGGACAGAGCTGGGCAGACACACGGGCATCCATGSGCTCCACCTTCTCCAGCACCACTC 840  
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QY 841 GGGCCCATCTTCTGGCTGCTGGTCAAGAGCCCCCGAGTGGCCGCCAGCCAGCACATAC 900  
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QY 901 CTGGCCGTGGCGAGGAATCTGGCGGATGTTTCCGGAAGTACTTTCGATGGACTCAAAACAG 960  
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QY 961 AAGGCCCGGCCCCCGAGGCTGAGGATGAGAGGTGGCCCGGAGGCTTTGGGCTGAAAGT 1020  
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QY 1021 GCGGCTGTGGTGGGCTTAGAGGCTCCCTCTGTGAGGAGCAGCCCCCTCCCCAGATAA 1080  
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QY 1081 CTGGAGCAGATTTGAAAGCCAGGATGGCGCTCCAGACCGAGGACAGCTGTCCGCCATGC 1140  
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QY 1141 CCGCAGCTTCTGGCACTACCTGAGCCGGGAGACCCAGACTGGCGCTGCAGGTGAGCACTGCC 1200  
Db |||||  
QY 1201 AGTAGGTTCTAGGGGCGGTGCTGGCCGAGTGGCTGAGGAGGAGGAGGAGGAGGAGGAG 1260  
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QY 1261 GGGCTCTGCTGTTCCGCTCTGCTGTGCCAGCAGGGGAGAGGGGCTCTGTGCACCTTGCAG 1320  
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      |||||

QY      1801  GCTCATTT 1808
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Db      1801  GCTCATTT 1808
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ID      ADD70630 standard; cDNA; 1808 BP.
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AC      ADD70630;
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DT      15-JAN-2004 (first entry)
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DE      Human cDNA encoding secreted/transmembrane protein PRO1430.
XX
KW      Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW      immune response; cardiac insufficiency disorder; calcium flux;
KW      umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW      arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW      Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW      dermatitis; herpetiformis; Crohn's disease; thalassaemia.
XX
OS      Homo sapiens.
XX
PN      US2003099625-A1.
XX
PD      29-MAY-2003.
XX
PF      12-DEC-2001; 2001US-00015386.
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PR 18-NOV-1998; 98US-0108849P.  
PR 18-NOV-1998; 98US-0108850P.  
PR 18-NOV-1998; 98US-0108851P.  
PR 18-NOV-1998; 98US-0108852P.  
PR 18-NOV-1998; 98US-0108858P.  
PR 18-NOV-1998; 98US-0108904P.  
PR 22-DEC-1998; 98US-0113296P.  
PR 30-DEC-1998; 98US-0114223P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 16-APR-1999; 99US-0129674P.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 15-SEP-1999; 99WO-US021194.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;  
XX  
DR WPI; 2003-874602/81.  
DR P-PSDB; ADD70631.  
XX  
PT Novel isolated PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555,  
PT PRO1787 affect glucose or free fatty acid (FFA) uptake by skeletal muscle  
PT cells and are useful for treating diabetes or hyper- or hypo-insulinemia.  
XX  
PS Claim 2; SEQ ID NO 115; 553pp; English.  
XX  
CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 1808; DB 9; Length 1808;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1808; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTACCCAGCGGCTGGTGTGACAGCAAGCTCCGCGCCGACTCCGACGCCTGACGCCT 60  
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DT 15-JAN-2004 (first entry)  
XX Human cDNA encoding secreted/transmembrane protein PRO1430.  
DE  
DE  
XX Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;  
KW immune response; cardiac insufficiency disorder; calcium flux;  
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;  
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;  
KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.  
XX  
OS Homo sapiens.  
XX  
XX US2003054406-A1.  
PN  
XX  
PD 20-MAR-2003.  
XX  
PF 06-DEC-2001; 2001US-00006818.  
XX  
PR 01-SEP-1998; 98US-0098716P.  
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PR 01-SEP-1998; 98US-0098750P.  
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99US-0129674P.





QY	1381	ACGTCAGAGAGCCAGCGGTGCCCTGTGCGGGAGGGTTCCAAGGTGCTCCGTGAAGAGCAT	1440
Db	1381	ACGTCAGAGAGAGCCAGCGGTGCCCTGTGCGGGAGGGTTCCAAGGTGCTCCGTGAAGAGCAT	1440
QY	1441	GGGCAAGTTGCTTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCTTGTGCATGCATG	1500
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QY	1501	GTCCCTCTCTGAGCCCTTGGTTTCTTCAGCAGTGAGATGCTCAGAATAACTGCTGTCTCCCA	1560
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QY	1561	TGATGGTGTGGTACAGCGAGCTGTTGTTCTTGGCTATGGCATGGCTGTCCGGGGTGTTC	1620
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QY	1621	CTGAGGGCTTCCTGTGCCAGAGCCAGCCAGAGCAGGTGCAGGTGTCATCCCGAGTTC	1680
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QY	1681	AGGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGTACAGGACCTGGGATTGC	1740
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QY	1741	CTGGGACTCCACCTTCCTATCAATTCTCATGGTAGTCCAAACTGCAGACTCTCAAATT	1800
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QY	1801	GCTCATTT	1808
Db	1801	GCTCATTT	1808

RESULT 10

ADD38274	ID	ADD38274 standard; cDNA; 1808 BP.
XX	AC	ADD38274;
XX	DT	15-JAN-2004 (first entry)
XX	DE	Human cDNA encoding secreted/transmembrane protein PRO1430.
XX	KW	Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
XX	KW	immune response; cardiac insufficiency disorder; calcium flux;
XX	KW	umbilical vein endothelial cell; bone disorder; cartilage disorder;
XX	KW	arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
XX	KW	Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
XX	KW	dermatitis; herpetiformis; Crohn's disease; thalassaemia.
OS		Homo sapiens.
XX	PN	US2003096955-A1.
XX	PD	22-MAY-2003.
XX	PF	07-DEC-2001; 2001US-00012755.
XX	PR	01-SEP-1998; 98US-0098716P.
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PR 23-JUN-1999; 99US-0141037P.  
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PR 01-SEP-1999; 99WO-US020111.  
PR 15-SEP-1999; 99WO-US021194.  
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PR 15-MAR-2000; 2000WO-US006884.  
PR 17-MAY-2000; 2000WO-US013705.  
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PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.  
XX PA (GETH ) GENENTECH INC.

XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;  
XX WPI; 2003-787000/74.  
DR P-PSDB; ADD38275.  
XX  
PT Novel isolated PRO polypeptide, useful for treating cancerous tumors,  
PT cardiac insufficiency disorders, wound healing, diabetes mellitus,  
PT thalassemias.  
XX  
PS Claim 2; SEQ ID NO 115; 556pp; English.  
XX  
CC The invention relates to an isolated PRO polypeptide (secreted or  
CC transmembrane protein) having at least 80% amino acid sequence identity  
Query Match 100.0%; Score 1808; DB 9; Length 1808;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1808; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCGCTGACGCCT 60  
DB 1 GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCGCTGACGCCT 60  
QY 61 GACGCCTGTCCCCGGCCCCGGCATGAGCCGCTACCTGCTGCCGCTGTCCGCGCTGGGCACG 120  
DB 61 GACGCCTGTCCCCGGCCCCGGCATGAGCCGCTACCTGCTGCCGCTGTCCGCGCTGGGCACG 120  
QY 121 GTAGCAGGCGCGCCGCTGCTCAAGGACTATGTCACCGGTGGGGCTTGCCCCAGCAAG 180  
DB 121 GTAGCAGGCGCGCCGCTGCTCAAGGACTATGTCACCGGTGGGGCTTGCCCCAGCAAG 180  
QY 181 GCCACCATCCCTGGGAAGACGGTCATCGTGACGSGCGCCAAACACAGGCATCGGGAAGCAG 240  
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QY 241 ACCGCCTTGGAACCTGGCCAGGAGAGGAGGCAACATCATCTGCGCTGCCGAGACATGGAG 300  
DB 241 ACCGCCTTGGAACCTGGCCAGGAGAGGAGGCAACATCATCTGCGCTGCCGAGACATGGAG 300  
QY 301 AAGTGTAGGCGGCAGCAAGGACATCCGCGGGGAGACCCTCAATCACCATGTCAACGCC 360  
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DB 541 ACAAACTTGCTGTGGACAGTGAAAGCCTCAGCCCTTCCGCGGATCATCAACCTCTCG 600  
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QY 721 CTGAGCGCGGGCTGCAAGGCTCTGGTGTGACTGTCAACGCCCTGCACCCCGCGGTGGCC 780  
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QY 781 AGGACAGAGCTGGGCAGACACACGGGCATCCATGGCTCCACCTTCTCCAGCACCACTC 840  
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QY 841 GGGCCCATCTTCTGGCTGTGGTCAAGAGCCCCGAGCTGGCGCCAGCCCCAGCACATAC 900  
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Db |||||

RESULT 11  
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AC ADD39230;  
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DT 15-JAN-2004 (first entry)  
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KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;  
KW immune response; cardiac insufficiency disorder; calcium flux;  
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;  
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;  
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.  
XX  
OS Homo sapiens.  
XX  
PN US2003096954-A1.  
PD 22-MAY-2003.  
XX  
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PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
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PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
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PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams FM, Wood WI;  
XX  
WPI; 2003-786999/74.  
DR P-PSDB; ADD39231.  
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XX  
PT Novel isolated PRO polypeptide useful for tissue typing, modulating  
PT biological activity of cell, as molecular weight markers in protein  
PT electrophoresis, for treating arthritis, tumor.  
XX  
PS Claim 2; SEQ ID NO 115; 550pp; English.  
XX  
CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 1808; DB 9; Length 1808;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1808; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT 15-JAN-2004 (first entry)  
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DE Human cDNA encoding secreted/transmembrane protein PRO1430.  
XX  
KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;  
KW immune response; cardiac insufficiency disorder; calcium flux;  
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;  
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;  
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.  
XX  
OS Homo sapiens.  
XX  
PN US2003092061-A1.  
XX  
PD 15-MAY-2003.  
XX  
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PR 28-FEB-2001; 2001WO-US006520.





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Qy      1801 GCTCATT 1808
Db      1801 GCTCATT 1808

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AC      ADD40184;
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KW      Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW      immune response; cardiac insufficiency disorder; calcium flux;
KW      umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW      arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW      Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW      dermatitis; herpeticformis; Crohn's disease; thalassaemia.
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AC	ADE50405;					98US-0100713P.
XX						98US-0100713P.
DT	29-JAN-2004 (first entry)					98US-0100713P.
XX						98US-0100713P.
DE	Human cDNA encoding secreted/transmembrane protein PRO1430.					98US-0100713P.
XX						98US-0100713P.
KW	Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;					98US-0100713P.
KW	immune response; cardiac insufficiency disorder; calcium flux;					98US-0100713P.
KW	umbilical vein endothelial cell; bone disorder; cartilage disorder;					98US-0100713P.
KW	arthritis; wound healing; diabetes; skeletal muscle cells; obesity;					98US-0100713P.
KW	Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;					98US-0100713P.
KW	dermatitis; herpeticiformis; Crohn's disease; thalassaemia.					98US-0100713P.
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PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;  
XX  
DR WPI; 2003-708395/67.  
DR P-PSDB; ADE50406.  
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PT Novel secreted and transmembrane PRO polypeptides useful in the  
PT preparation of a medicament for treating a condition responsive to PRO  
PT polypeptide and as therapeutic agents e.g. vaccines.  
XX  
PS Claim 2; SEQ ID NO 115; 555pp; English.  
XX  
CC The invention relates to an isolated PRO polypeptide (secreted or  
Query Match 100.0%; Score 1808; DB 9; Length 1808;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1808; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 901 CTGGCCGTGGCGAGGAACTGGCGGATGTTTCCGGAAGTACTTCGATGGACTCAAACAG 960  
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QY 961 AAGGCCCGGCCCGGAGGCTGAGGATCAGAGGTGGCCCGAGGCTTTGGGCTGAAAGT 1020  
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QY 1021 GCCCGCTGGTGGCTTAGAGGCTCCCTCTGTGAGGGAGCAGCCCTCCCCAGATAACT 1080  
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Db 1081 CTGGAGCAGATTGAAAGCCAGGATGGCGCTCCAGACCGAGGACAGCTGTCCGCCATGC 1140  
QY 1141 CCGCAGCTTCTGGGCACTACCTGAGCCGGAGACCCAGGACTGGCGGCCGCCATGCCGC 1200  
Db 1141 CCGCAGCTTCTGGGCACTACCTGAGCCGGAGACCCAGGACTGGCGGCCGCCATGCCGC 1200  
QY 1201 AGTAGGTTCTAGGGGCGGTGCTGGCCGAGTGGAAGTGGCCCTGAGGAGGAGGAGGAGG 1260  
Db 1201 AGTAGGTTCTAGGGGCGGTGCTGGCCGAGTGGAAGTGGCCCTGAGGAGGAGGAGGAGG 1260  
QY 1261 GGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAGAGGGGCCATCTGATGCTT 1320  
Db 1261 GGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAGAGGGGCCATCTGATGCTT 1320  
QY 1321 CCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAGGGGCTCTGTGCACTTGCAGGCC 1380  
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QY 1381 ACGTCAGGAGAGCCAGCGGTGCCCTGTCCGGGAGGGTTCCAAGGTGCTCCGTGAAGAGCAT 1440  
Db 1381 ACGTCAGGAGAGCCAGCGGTGCCCTGTCCGGGAGGGTTCCAAGGTGCTCCGTGAAGAGCAT 1440  
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QY 1501 GTCCTCTCTGAGCCCTGGTTTCTTCAAGAGTGAGATGCTCAGATAAAGTCTGTCTCCCA 1560  
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QY 1621 CTGAGGGCTTCTGTGCCAGAGCCCGAGGAGCAGGTGAGGTGTCATCCCGAGTTC 1680

Db 1621 CTGAGGGCTTCTGTGCCAGAGCCAGCCAGAGCAGGTGTCAGGTGTATCCCGAGTTC 1680  
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Db 1801 GCTCATTT 1808

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XX  
DT 29-JAN-2004 (first entry)  
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KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;  
KW immune response; cardiac insufficiency disorder; calcium flux;  
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;  
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;  
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.  
XX Homo sapiens.  
OS  
PN US2003092883-A1.  
XX  
PD 15-MAY-2003.  
XX  
PF 10-DEC-2001; 2001US-00013430.  
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PR 01-SEP-1998; 98US-0098723P.  
PR 01-SEP-1998; 98US-0098749P.  
PR 01-SEP-1998; 98US-0098750P.  
PR 02-SEP-1998; 98US-0098803P.  
PR 02-SEP-1998; 98US-0098821P.  
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PR 16-SEP-1998; 98US-0100627P.  
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PR 16-SEP-1998; 98US-0100664P.  
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PR 17-SEP-1998; 98US-0100919P.

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PR	06-OCT-1998;	98US-0103258P.	PR	06-JAN-2000;	2000WO-US000376.
PR	06-OCT-1998;	98US-0103449P.	PR	11-FEB-2000;	2000WO-US003565.
PR	07-OCT-1998;	98US-0103314P.	PR	18-FEB-2000;	2000WO-US004342.
PR	07-OCT-1998;	98US-0103315P.	PR	24-FEB-2000;	2000WO-US005004.
PR	07-OCT-1998;	98US-0103328P.	PR	02-MAR-2000;	2000WO-US005841.
PR	07-OCT-1998;	98US-0103395P.	PR	15-MAR-2000;	2000WO-US006884.
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PR	08-OCT-1998;	98US-0103678P.	PR	02-JUN-2000;	2000WO-US015264.
PR	08-OCT-1998;	98US-0103679P.	PR	23-AUG-2000;	2000WO-US023522.
PR	08-OCT-1998;	98US-0103711P.	PR	24-AUG-2000;	2000WO-US023328.
PR	14-OCT-1998;	98US-0104257P.	PR	08-NOV-2000;	2000WO-US030952.
PR	20-OCT-1998;	98US-0104987P.	PR	10-NOV-2000;	2000WO-US030873.
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PR	22-OCT-1998;	98US-0105169P.	PR	01-JUN-2001;	2001WO-US017800.
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PR	27-OCT-1998;	98US-0105881P.	XX		
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PR	27-OCT-1998;	98US-0106062P.	XX		
PR	28-OCT-1998;	98US-0106023P.	PI	Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;	
PR	28-OCT-1998;	98US-0106029P.	PI	Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;	
PR	28-OCT-1998;	98US-0106030P.	PI	Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;	
PR	28-OCT-1998;	98US-0106032P.	PI	Williams PM, Wood WI;	
PR	28-OCT-1998;	98US-0106033P.	XX		
PR	28-OCT-1998;	98US-0106178P.	DR	WPI; 2003-765493/72.	
PR	29-OCT-1998;	98US-0106248P.	DR	P-PSDB; ADE20018.	
PR	29-OCT-1998;	98US-0106384P.	XX		
PR	29-OCT-1998;	98US-0108500P.	PT	New isolated PRO polypeptide useful for tissue typing, modulating	
PR	30-OCT-1998;	98US-0106464P.	PT	biological activity of cell, as molecular weight markers in protein	
PR	03-NOV-1998;	98US-0108856P.	PT	electrophoresis, for treating arthritis and tumors.	
PR	03-NOV-1998;	98US-0106902P.	XX		
PR	03-NOV-1998;	98US-0106905P.	PS	Claim 2; SEQ ID NO 115; 555pp; English.	
PR	03-NOV-1998;	98US-0106919P.	XX		
PR	03-NOV-1998;	98US-0106932P.	CC	The invention relates to an isolated PRO polypeptide (secreted or	
PR	03-NOV-1998;	98US-0106934P.			100.0%; Score 1808; DB 9; Length 1808;
PR	10-NOV-1998;	98US-0107783P.		Query Match	



Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1808; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	GAGTACCCAGCGGCTGGTGTGCAGCAAGCTCCGGCCGACTCCGGACGCCTGACGCCT	60						
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QY	121	GTAGCAGCGCCCGCTGTGCTCAAGGACTATGTACCCGGTGGGCTTGCCCCAGCAAG	180						
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QY	181	GCACCATCCCTGGGAAGACGGTTCATCGTAGCGGGCCCAACACAGGCATCGGGAAGCAG	240						
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QY	241	ACCGCTTGGAACCTGGCCAGGAGAGGAGGCAACATCATCTGGCCTGCCGAGACATGGAG	300						
Db	241	ACCGCTTGGAACCTGGCCAGGAGAGGAGGCAACATCATCTGGCCTGCCGAGACATGGAG	300						
QY	301	AAGTGTAGGCGGCAGCAAGACATCCGCGGGAGACCCTCAATCACCATGTCAACGCC	360						
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QY	361	CGCACCTGGACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAAAGATCATTTAA	420						
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QY	421	GAGGAGGCGAGTGGACATTTCTAATCAACACGCGGGTGTGATCGGTCGCCCACTGG	480						
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QY	481	ACCACCGAGGACGGCTTCGAGATGCAGTTTGGCGTTTACCACCTGGTCACTTCTCTTG	540						
Db	481	ACCACCGAGGACGGCTTCGAGATGCAGTTTGGCGTTTACCACCTGGTCACTTCTCTTG	540						
QY	541	ACAACTTGTCTGTGGACAAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCG	600						
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QY	601	TCCCTGSCCATGTTGCTGGGCACATAGACTTTGACGACTTGAACCTGGCAGACAGGAAG	660						
Db	601	TCCCTGSCCATGTTGCTGGGCACATAGACTTTGACGACTTGAACCTGGCAGACAGGAAG	660						
QY	661	TATAACCAAAAGCCGCTACTGCCAGAGCAAGCTCGCCATCGTCTCTTCAACCAAGGAG	720						
Db	661	TATAACCAAAAGCCGCTACTGCCAGAGCAAGCTCGCCATCGTCTCTTCAACCAAGGAG	720						
QY	721	CTGAGCCGGCGGTGCAAGGCTCTGGTGTGACTGTCAACGCCCTGCACCCCGGCTGGCC	780						
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QY	781	AGGACAGAGCTGGGCAGACACACGGGCATCCATGGCTCCACCTTCTCCAGCACCACTC	840						
Db	781	AGGACAGAGCTGGGCAGACACACGGGCATCCATGGCTCCACCTTCTCCAGCACCACTC	840						
QY	841	GGGCCCCATCTTCTGGCTGTGGTCAAGAGCCCCGAGCTGGCGCCCGCCAGCATACTAC	900						
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QY	901	CTGGCCGTGGCGAGGAACTGGCGGATGTTTCCGGAAGTACTTCGATGGACTCAACAG	960						
Db	901	CTGGCCGTGGCGAGGAACTGGCGGATGTTTCCGGAAGTACTTCGATGGACTCAACAG	960						
QY	961	AAGGCCCGGCCCGGAGGCTGAGGATGAGGAGGTGGCCCGAGGCTTTGGGCTGAAAGT	1020						
Db	961	AAGGCCCGGCCCGGAGGCTGAGGATGAGGAGGTGGCCCGAGGCTTTGGGCTGAAAGT	1020						
QY	1021	GCCCGCTGGTGGGCTTAGAGGCTCCCTCTGTGAGGGAGCAGCCCTCCCCAGATAACCT	1080						

Db	1021	GCCCGCTGGTGGGCTTAGAGGCTCCCTCTGTGAGGGAGCAGCCCTCCCCAGATAACCT	1080
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QY	1681	AGGCTCTGCACGGCATGGAGTGGGAACCCACAGCTGTCTACAGGACCTGGGATTGC	1740
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Search completed: June 23, 2004, 11:23:33  
Job time : 743 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
Run on: June 23, 2004, 11:04:51 ; Search time 7182 Seconds  
(without alignments)  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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8: gb\_pl:  
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30: em\_htg\_hum:  
31: em\_htg\_inv:  
32: em\_htg\_other:  
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41: em\_htgo\_other:

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1792	99.1	1878	6	AX136157	AX136157 Sequence
4	1792	99.1	1878	6	BD123531	BD123531 Secretary
5	1792	99.1	1878	9	AK075392	AK075392 Homo sapi
6	1647.6	91.1	2006	9	BC009881	BC009881 Homo sapi
7	1259.4	69.7	3055	9	AK122764	AK122764 Homo sapi
8	1231.4	68.1	1282	6	AX195176	AX195176 Sequence
9	1189.8	65.8	1699	6	AX179293	AX179293 Sequence
C 10	966.4	53.5	204340	2	AC019238	AC019238 Homo sapi
C 11	963.2	53.3	187064	9	AC011476	AC011476 Homo sapi
12	916.8	50.7	1153	6	AX179291	AX179291 Sequence
C 13	500	27.7	554	6	AX136638	AX136638 Sequence
C 14	500	27.7	554	6	BD123878	BD123878 Secretary
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ALIGNMENTS

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LOCUS AX697047 1808 bp DNA linear PAT 02-APR-2003  
DEFINITION Sequence 115 from Patent WO0078961.  
ACCESSION AX697047  
VERSION AX697047.1 GI:29498030  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS  
1 Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L.,  
Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A.,  
Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,

Pred. No. is the number of results predicted by chance to have a

TITLE Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
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JOURNAL Patent: WO 0078961-A 115 28-DEC-2000;  
Genentech Inc. (US)  
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ACCESSION AY358473

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 AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.  
 TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment  
 JOURNAL Genome Res. 13 (10), 2265-2270 (2003)  
 PUBMED 12975309  
 REFERENCE 2 (bases 1 to 1808)  
 AUTHORS Clark,H.F.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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ACCESSION AX136157
VERSION AX136157.1 GI:14272565
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.
TITLE Secretory protein or membrane protein
JOURNAL Patent: Ep 1067182-A 79 10-JAN-2001;
Helix Research Institute (JP)
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LOCUS Secretory protein or membrane protein.  
DEFINITION Secretory protein or membrane protein.  
ACCESSION BD123531  
VERSION BD123531.1 GI:23218476  
KEYWORDS JP 2002017376-A/40.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo..  
REFERENCE 1 (bases 1 to 1878)  
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.  
TITLE Secretory protein or membrane protein  
JOURNAL Patent: JP 2002017376-A 40 22-JAN-2002;  
COMMENT HELIX RESEARCH INSTITUTE  
OS Homo sapiens (human)  
PN JP 2002017376-A/40  
PD 22-JAN-2002  
PF 07-JUL-2000 JP 2000253173  
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,TOMOYASU

PI SUGIYAMA,  
PI KOJI HAYASHI  
PC  
C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC  
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Db 1871 GCTCATTT 1878

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AK075392 1878 bp mRNA linear PRI 03-SEP-2002

LOCUS Homo sapiens cDNA PSEC0082 fis, clone NT2RP2004966, weakly similar

DEFINITION to PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).

ACCESSION AK075392

VERSION AK075392.1 GI:22761450

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Ota, T., Nishikawa, T., Suzuki, Y., Kawai-Hio, Y., Hayashi, K., Ishii, S., Saito, K., Yamamoto, J., Wakamatsu, A., Nagai, T., Nakamura, Y., Nagahari, K., Sugano, S. and Isogai, T. HRI human cDNA sequencing project

AUTHORS Unpublished

TITLE 2 (bases 1 to 1878)

JOURNAL Isogai, T. and Yamamoto, J.

REFERENCE Direct Submission

AUTHORS Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)

TITLE HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass

JOURNAL sequencing, clone selection and full insert sequencing: Helix Research Institute (supported by Japan Key Technology Center etc.);

AUTHORS Research Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center.

FEATURES

source Location/Qualifiers

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152..1147

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CDS

ORIGIN

Query Match 99.1%; Score 1792; DB 9; Length 1878;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 1798; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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RESULT 6

BC009881

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

BC009881

Homo sapiens retinol dehydrogenase 13 (all-trans and 9-cis), mRNA

(cDNA clone MGC:16483 IMAGE:3956119), complete cds.

BC009881

BC009881.2

GI:33872511

MGC.

Homo sapiens (human)

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2006)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Biakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 2006)

AUTHORS	Strausberg,R.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>
COMMENT	On Aug 19, 2003 this sequence version replaced gi:14602729. Contact: MGC help desk Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a> Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology <a href="http://www.systemsbiology.org">http://www.systemsbiology.org</a> contact: <a href="mailto:amadan@systemsbiology.org">amadan@systemsbiology.org</a> Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Series: IRAL Plate: 25 Row: k Column: 11 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19923930.	
FEATURES	Location/Qualifiers
source	1..2006 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:16483 IMAGE:3956119" /tissue_type="Placenta, choriocarcinoma" /clone_lib="NIH MGC 21" /lab_host="DH10B-R" /note="vector: potB7"
gene	1..2006 /gene="RDH13"
CDS	475..1257 /codon_start=1 /product="retinol dehydrogenase 13 (all-trans and 9-cis)" /protein_id="AAH09881.1" /db_xref="GI:14602730" /db_xref="LocusID:112724" /translation="MEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEE SLVDILINAGVMRCPHWTTEDGFEMQFVGNHLGFLTLNLLDLKLSAPSRIINLS ERLHVAGHIDFDLNLWQTKYNTKAYCOSKLAIVLFTKLSRRLOQSGVTVNALHPG VARTELGRHTGIHGSTFSSTLGLPIFWLLVKSPELAAQSTYLAVAEELADVSGKYFD GLKQKAPAEAEDEEVARRLWAEARLVGLEAPSVREQPLPR" 478..1110 /note="adh short; Region: short chain dehydrogenase. This family contains a wide variety of dehydrogenases" /db_xref="CDD:pfam00106"
ORIGIN	Query Match 91.1%; Score 1647.6; DB 9; Length 2006; Best Local Similarity 99.7%; Pred. No. 1.9e-301; Matches 1661; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  Qy 144 CAAGGACTATGTACCGGTGGGGCTTGCCCGCAGCAAGGCCACCATCCCTGGGAAGACGGT 203 Db       Qy 323 CAGGGACTATGTACCGGTGGGGCTTGCCCGCAGCAAGGCCACCATCCCTGGGAAGACGGT 382 Db       Qy 204 CATCGTGACGGGCGCCACACAGGCATCGGGAAGCAGACCGCCTTGGAAC-TGGCCAGGA 262 Db       Qy 383 CATCGTGACGGGCGCCACACAGGCATCGGGAAGCAGACCGCCTTGGAACCTGGCCAGGA 442 Db       Qy 263 GAGGAGCAACATCATCTTGGCTGCCGAGACATGGAGAAGTGTAGCGGCGCAGCAAGG 322 Db       Qy 443 GAGGAGCAACATCATCTTGGCTGCCGAGACATGGAGAAGTGTAGCGGCGCAGCAAGG 502 Db       Qy 323 ACATCCGGGGGAGACCCCTCAATCACCATGTCAACGCCCGGCACCTGGACTTGGCTTCCC 382 Db       Qy 503 ACATCCGGGGGAGACCCCTCAATCACCATGTCAACGCCCGGCACCTGGACTTGGCTTCCC 562 Db

Qy	383	TCAAGTCTATCCGAGAGTTTGCAGCAAAAGATCATTTGAAGAGGAGGAGCGAGTGGACATTC	442
Db	563	TCAAGTCTATCCGAGAGTTTGCAGCAAAAGATCATTTGAAGAGGAGGAGCGAGTGGACATTC	622
Qy	443	TAATCAACAACCGGGGTGTGATGCGGTGCCCCCCTGAGACCCAGGAGGACGGCTTCGAGA	502
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Qy	503	TGCAGTTTGGCGTTAACCACTGGGTCACTTTCTCTTGACAAACTTGTCTGTCGACAAGC	562
Db	683	TGCAGTTTGGCGTTAACCACTGGGTCACTTTCTCTTGACAAACTTGTCTGTCGACAAGC	742
Qy	563	TGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCCATGTTGCTGGGC	622
Db	743	TGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCCATGTTGCTGGGC	802
Qy	623	ACATAGACTTTGACGACTTGAACTGGCAGACGAGGAAGTATAACACCAAGCCGCTACT	682
Db	803	ACATAGACTTTGACGACTTGAACTGGCAGACGAGGAAGTATAACACCAAGCCGCTACT	862
Qy	683	GCCAGAGCAAGCTGCCCATCGTCTCTTACCAAGGAGCTGAGCGCGGCTGCAAGGCT	742
Db	863	GCCAGAGCAAGCTGCCCATCGTCTCTTACCAAGGAGCTGAGCGCGGCTGCAAGGCT	922
Qy	743	CTGGTGTGACTGTCAACGCCCTTGACCCCGCGTGGCCAGGACAGAGCTGGGCAGACACA	802
Db	923	CTGGTGTGACTGTCAACGCCCTTGACCCCGCGTGGCCAGGACAGAGCTGGGCAGACACA	982
Qy	803	CGGGCATCCATGGCTCCACCTTCTCCAGCACCACTCGGGGCCATCTTCTGGCTGCTGG	862
Db	983	CGGGCATCCATGGCTCCACCTTCTCCAGCACCACTCGGGGCCATCTTCTGGCTGCTGG	1042
Qy	863	TCAAGAGCCCCGAGCTGGCGCCCCAGCCAGCACACATACCTGGCGTGGCGGAGGAACTGG	922
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Qy	983	AGGATGAGGAGTGCGCCCCGAGGCTTTGGGCTGAAAGTGCCCGCTGGTGGGCTTAGAGG	1042
Db	1163	AGGATGAGGAGTGCGCCCCGAGGCTTTGGGCTGAAAGTGCCCGCTGGTGGGCTTAGAGG	1222
Qy	1043	CTCCCTCTGTGAGGAGCAGCCCCCTCCAGATAAACCTCTGGAGCAGATTTGAAAGCCAG	1102
Db	1223	CTCCCTCTGTGAGGAGCAGCCCCCTCCAGATAAACCTCTGGAGCAGATTTGAAAGCCAG	1282
Qy	1103	GATGGCGCCTCCAGACCGAGGACAGCTGTCGCCCATGCCCGCAGCTTCTGGCCTACCT	1162
Db	1283	GATGGCGCCTCCAGACCGAGGACAGCTGTCGCCCATGCCCGCAGCTTCTGGCCTACCT	1342
Qy	1163	GAGCCGGGAGACCCAGGACTGGCGCGCCCATGCCCGAGTAGGTTCTAGGGGGCGGTGC	1222
Db	1343	GAGCCGGGAGACCCAGGACTGGCGCGCCCATGCCCGAGTAGGTTCTAGGGGGCGGTGC	1402
Qy	1223	TGGCCGAGTGAGTGGCTTCAGGTGAGCACTGCCCGGGCTCTGGCTGGTTCGGTCTG	1282
Db	1403	TGGCCGAGTGAGTGGCTTCAGGTGAGCACTGCCCGGGCTCTGGCTGGTTCGGTCTG	1462
Qy	1283	CTCTGCTGCCAGCAGGGGAGAGGGCCATCTGATGCTTCCCTGGGAATCTAAACTGGGA	1342
Db	1463	CTCTGCTGCCAGCAGGGGAGAGGGCCATCTGATGCTTCCCTGGGAATCTAAACTGGGA	1522
Qy	1343	ATGGCCGAGGAGGAAGGGCTCTGTGCATTTGACGTCAGGCGCCACGTCAGGAGCGCGGTGC	1402
Db	1523	ATGGCCGAGGAGGAAGGGCTCTGTGCATTTGACGTCAGGCGCCACGTCAGGAGCGCGGTGC	1582
Qy	1403	CTGTCTGGGGAGGGTTCCAAGGTGCTCCGTGAAGAGCATGGGCAAGTTGTGTGACACTTGG	1462
Db	1583	CTGTCTGGGGAGGGTTCCAAGGTGCTCCGTGAAGAGCATGGGCAAGTTGTGTGACACTTGG	1642



QY 1463 TGGATTCTTGGGTCCCTGTGGGACCTTGTGATGCATGGTCTCTCTGAGCCTTGGTTTC 1522  
Db |||||||  
QY 1643 TGGATTCTTGGGTCCCTGTGGGACCTTGTGATGCATGGTCTCTCTGAGCCTTGGTTTC 1702  
Db |||||||  
QY 1523 TTCAGCAGTGAGATGCTCAGAAATAACTGCTGTCTCCCATGATGGTGTGGTACAGCGAGCT 1582  
Db |||||||  
QY 1703 TTCAGCAGTGAGATGCTCAGAAATAACTGCTGTCTCCCATGATGGTGTGGTACAGCGAGCT 1762  
Db |||||||  
QY 1583 GTTGTCTGGCTATGGCATGGCTGTGCCCCGGGGTGTGCTGAGGGCTTCTGTGCCAGAG 1642  
Db |||||||  
QY 1763 GTTGTCTGGCTATGGCATGGCTGTGCCCCGGGGTGTGCTGAGGGCTTCTGTGCCAGAG 1822  
Db |||||||  
QY 1643 CCCAGCCAGAGAGCAGGTGCAGGTGTCTATCCCGAGTTTCAGGCTCTGCACGGCATGGAGTG 1702  
Db |||||||  
QY 1823 CCCAGCCAGAGAGCAGGTGCAGGTGTCTATCCCTGAGTTCAGGCTCTGCACGGCATGGAGTG 1882  
Db |||||||  
QY 1703 GGAACCCACCAGCTGCTGTCTACAGGACCTGGGATTCCTGGGACTCCACCTTTCCTATC 1762  
Db |||||||  
QY 1883 GGAACCCACCAGCTGCTGTCTACAGGACCTGGGATTCCTGGGACTCCACCTTTCCTATC 1942  
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QY 1763 AATTCTCATGTTAGTCCAAACTGCAGACTCTCAAACTTGCTCAATT 1808  
Db |||||||  
QY 1943 AATTCTCATGTTAGTCCAAACTGCAGACTCTCAAACTTGCTCAATT 1988  
Db |||||||

RESULT 7  
AK122764 3055 bp mRNA linear PRI 09-SEP-2003  
LOCUS Homo sapiens cDNA FLJ16300 fis, clone PLACE7000167, moderately  
DEFINITION similar to Homo sapiens androgen-regulated short-chain  
dehydrogenase/reductase 1 (ARSDR1) mRNA.

ACCESSION AK122764  
VERSION AK122764.1 GI:34527960  
KEYWORDS oligo capping; fis (full insert sequence).  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 Tashiro,H., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S.,  
Fukuzumi,Y., Fujimori,Y., Komiyama,M., Sugiyama,T., Irie,R.,  
Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,  
Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,  
Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,  
Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,  
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,  
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.  
NEDO human cDNA sequencing project

TITLE Unpublished  
JOURNAL 2 (bases 1 to 3055)  
REFERENCE Isogai,T. and Yamamoto,J.  
AUTHORS Direct Submission  
TITLE Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7  
JOURNAL Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan  
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of  
Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
Research Association for Biotechnology (RAB); cDNA library  
construction: Helix Research Institute (HRI) (supported by Japan  
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,  
HRI, and Biotechnology Center, National Institute of Technology and  
Evaluation; clone selection for full insert sequencing: HRI and  
RAB; annotation: HRI and RAB.  
FEATURES Location/Qualifiers  
source 1.3055  
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/clone="PLACE7000167"  
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ORIGIN

Query Match 69.7%; Score 1259.4; DB 9; Length 3055;  
Best Local Similarity 77.8%; Pred. No. 4.6e-228;  
Matches 1797; Conservative 0; Mismatches 11; Indels 501; Gaps 3;  
QY 1 GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCG-----GACGCCT 53  
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QY 54 GACGCCTGACGCCTGTCCCCGGCCCGGCATGAGCCGCTACCTGTGCGGTGTGGCGCT 113  
Db GACGCCTGACGCCTGTCCCCGGCCCGGCATGAGCCGCTACCTGTGCGGTGTGGCGCT 847  
QY 114 GGGCACGGTAGCAGGCGCGCCCGTGTCTCTCAAGGACTATGTACCGGTGGGGCTTGCCC 173  
Db GGGCACGGTAGCAGGCGCGCCCGTGTCTCTCAAGGACTATGTACCGGTGGGGCTTGCCC 907  
QY 174 CAGCAAGGCCACCATCCCTGGGAGACGGTCTATCGTGACGGGCGCAATACAGGCATCGG 233  
Db CAGCAAGGCCACCATCCCTGGGAGACGGTCTATCGTGACGGGCGCAATACAGGCATCGG 967  
QY 234 GAAGCAGACCGCCTTGGAACTGGCCAGGAGGAGGCAACATCATCTGGCTGCCGAGA 293  
Db GAAGCAGACCGCCTTGGAACTGGCCAGGAGGAGGCAACATCATCTGGCTGCCGAGA 1027  
QY 294 CATGGAGAAAGTGTGAGCGGCGCAGCAAAAGGACATCCCGGGGAGACCCCTCAATCACCATGT 353  
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QY 414 CATTGAAGAGGAGGAGCGAGTGGACATTCTTAATCAACAACGCGGGTGTGATGCGGTGCCCC 473  
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QY 474 CCACTGGACCAACCGAGGACGGCTTCGAGATGCGAGTTTGGCGTTAACCCACTGGGTCACTT 533  
Db CCACTGGACCAACCGAGGACGGCTTCGAGATGCGAGTTTGGCGTTAACCCACTGGGTCACTT 1267  
QY 534 TCTCTTGACAAACTTGTCTGCTGGACAAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAA 593  
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QY 654 GAGGAAGTATAACACCAAGCCGCCCTACTGCCAGAGCAAGCTCGCCATCGTCTCTTTCAC 713  
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QY 740 ----- 739  
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QY 1568 CACTAATCGATCGTTTCTCTGAGGATTGTCTGTTATCCAGGTGGTCTAGTCTGCTGG 1627  
Db -----GC 741  
QY 1628 ATCAGATGTCCTTCCCTGTGTGTGTTGGCAGGCAGCTCAGCCTTTTGGCTCCAGCCAGC 1687  
Db -----GC 741  
QY 742 TCTGTGTGACTGTCAACGCGCCTGCACCCCGCGGTGGCAGGACAGAGCTGGGCGAGACAC 801  
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QY 421 GAGGAGGAGGAGTGGACATTTCTAATCAACAAACCGCGGCTGTGATGCGGTGCCCCACTGG 480  
Db 470 GAGGAGGAGGAGTGGACATTTCTAATCAACAAACCGCGGCTGTGATGCGGTGCCCCACTGG 529  
QY 481 ACCACCGAGGAGGCTTCGAGATGAGTTTGGCGTTTAAACCACTGGGTCACTTCTCTTG 540  
Db 530 ACCACCGAGGAGGCTTCGAGATGAGTTTGGCGTTTAAACCACTGGGTCACTTCTCTTG 589  
QY 541 ACAAACTTGTCTGGCAAGCTGAAAGCCTCAGCCCTTCGCGGATCATCAACCTCTCG 600  
Db 590 ACAAACTTGTCTGGCAAGCTGAAAGCCTCAGCCCTTCGCGGATCATCAACCTCTCG 649  
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Db 650 TCCCTGGCCCATGTTGCTGGCACATAGACTTTGACGACTTGAACCTGACAGGAGGAG 709  
QY 661 TATAACACCAAGCCGCTACTGCGCAGAGCAAGCTGCGCATGCTCTCTTCAACCAAGGAG 720  
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QY 721 CTGAGCCGCGGCTGCAAGGCTCTGCTGTGACTGTCAACGCGCTGCACCGCGGTGGCC 780  
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QY 781 AGGACAGAGCTGGGAGGAGCAACAGGCGCATCCATGCTTCCACCTTCTCCAGCACCACATC 840  
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QY 961 AAGGCCCGGCGGCGGAGGAGTGGAGGAGTGGCGCGCGGAGGCTTGGGCTGAAAGT 1020  
Db 1010 AAGGCCCGGCGGCGGAGGAGTGGAGGAGTGGCGCGCGGAGGCTTGGGCTGAAAGT 1069  
QY 1021 GCCCGCTGGTGGCTTAGAGCTCCCTCTGTGAGGAGGAGCGCCCTCCCGCAGATAACCT 1080  
Db 1070 GCCCGCTGGTGGCTTAGAGCTCCCTCTGTGAGGAGGAGCGCCCTCCCGCAGATAACCT 1129  
QY 1081 CTGAGCAGATTTGAAAGCCAGGATGGCGCTCCAGACCCGAGGACAGCTGTCGCCATGC 1140  
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QY 1141 CCGCAGCTTCTGGCACTACTGAGCCGGGAGACCCAGGACTGGCGCGCCCATGCCCGC 1200  
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Db 1250 AGTAGTTCTAGGGGCGGTGCTGGCGCAGTG 1282

RESULT 9  
AX179293  
LOCUS AX179293 1699 bp DNA linear PAT 03-JUL-2001  
DEFINITION Sequence 6 from Patent WO014446.  
ACCESSION AX179293  
VERSION AX179293.1 GI:14598963  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Meyers, R.  
TITLE 21612, 21615, 21620, 21676, 33756, novel human alcohol  
dehydrogenases

JOURNAL Patent: WO 0144446-A 6 21-JUN-2001;  
Millennium Pharmaceuticals, Inc. (US)  
FEATURES Location/Qualifiers  
source 1.1699  
CDS  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
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ORIGIN  
Query Match 65.8%; Score 1189.8; DB 6; Length 1699;  
Best Local Similarity 99.8%; Pred. No. 7.2e-215;  
Matches 1191; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GAGCTACCCAGCGCGCTGGTGTGTCAGCAAGCTCCGCGCGGACTCCGCGCGCTGACGCCT 60  
Db 457 GAGCTACCCAGCGCGCTGGTGTGTCAGCAAGCTCCGCGCGGACTCCGCGCGCTGACGCCT 516  
QY 61 GACGCTGTCCCGCGCGCGCGGATGAGCGGCTACCTGCTGCGGCTGTGCGGCTGGGCACG 120  
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QY 121 GTAGCAGCGCGCGCGCTGCTGCTCAAGGACTATGTCAACCGGTGGGCTTGGCCCAAG 180  
Db 577 GTAGCAGCGCGCGCGCTGCTGCTCAAGGACTATGTCAACCGGTGGGCTTGGCCCAAG 636  
QY 181 GCCACCATCCCTGGGAAGACGGTCACTGTGACGCGCGGCGCAACACAGGATCGGGAAGCAG 240  
Db 637 GCCACCATCCCTGGGAAGACGGTCACTGTGACGCGCGGCGCAACACAGGATCGGGAAGCAG 696  
QY 241 ACCGCTTGGAACTGGCCAGGAGAGGAGGCAACATCATCTGGCTGCGGAGACATGGAG 300  
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QY 301 AAGTGTGAGCGCGGAGCAAAAGGACATCCGCGGCGGAGACCCCTCAATCACCATGTCAACGCC 360  
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QY 361 CGGCACCTGGACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAGATCATTTGAA 420  
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Db 1057 TCCCTGGCCCATGTTGCTGGGCACATAGACTTTGACGACTTGAACCTGCGGATCATCAACCTCTCG 1116  
QY 661 TATAACACCAAGCCGCTACTGCGCAGAGCAAGCTCGCCATCGTCTCTTCAACCAAGGAG 720  
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Best Local Similarity 99.9%; Pred. No. 6.8e-173; Matches 967; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
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QY	901	CTGGCCGTGGCGGAGGAACCTGGCGGATGTTTCCGGAAGTACTTCGATGGACTCAAAACAG	960	
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QY	961	AAGGCCCGCCCCCGAGGCTGAGGATGAGGAGTGGCCCGAGGCTTTGGGCTGAAAGT	1020	
Db	93999	AAGGCCCGCCCCCGAGGCTGAGGATGAGGAGTGGCCCGAGGCTTTGGGCTGAAAGT	93940	
QY	1021	GCCCGCTGTGGCTTAGAGGCTCCCTCTGTGAGGGAGCAGCCCCCTCCCCAGATAACCT	1080	
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QY	1081	CTGGAGCAGATTGAAGCCAGGATGGCGCCTCCAGACCCGAGCAGCTGTCCGCCATGC	1140	
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QY	1261	GGGCTCTGGCTGTTCGGTCTGCTCTGCTGCCAGCAGGGAGAGGGCCATCTGATGCTT	1320	
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QY	1321	CCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTCTGTGCACTTGACGCC	1380	
Db	93639	CCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTCCGTGCACTTGACGCC	93580	
QY	1381	ACGTACGAGAGCCAGCGGTGCCCTGTCGGGAGGGTTCCAAGTGCTCCGTGAAGAGCAT	1440	
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QY	1441	GGGCAAGTTGTGTGACACTTGGTGGATCTTGGTCCCTGTGGACCTTGTGCAATGCATG	1500	
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QY	1501	GTCCCTCTGAGCCCTTGGTTTCTTCAGCAGTGAGATGCTCAGAATAACTGCTGTCTCCCA	1560	
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QY	1621	CTGAGGGCTTCCTGTGCCAGAGCCCGAGCAGAGCAGGTGCAGGTGTCTATCCCGAGTTC	1680	
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QY	1681	AGGCTCTGCACGGCATGGAGTGGGAACCCACACAGCTGCTGTACAGGACCTGGGATTC	1740	
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Db	93159	GCTCATTTT 93152		

RESULT 11

AC011476/c  
LOCUS AC011476 187064 bp DNA linear PRI 16-AUG-2002  
DEFINITION Homo sapiens chromosome 19 clone CTC-550B14, complete sequence.  
AC011476  
AC011476  
AC011476.8 GI:22267569  
HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 187064)  
DOE Joint Genome Institute and Stanford Human Genome Center.  
Direct Submision  
Unpublished  
2 (bases 1 to 187064)  
DOE Joint Genome Institute.  
Direct Submision  
Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
3 (bases 1 to 187064)  
DOE Joint Genome Institute and Stanford Human Genome Center.  
Submitted (16-AUG-2002) DOE Joint Genome Institute, 2800 Mitchell  
Drive, Walnut Creek, CA 94598, USA  
On Aug 16, 2002 this sequence version replaced gi:15022008.  
Draft Sequence Produced by DOE Joint Genome Institute  
www.jgi.doe.gov  
Finishing Completed at Stanford Human Genome Center  
www.shgc.stanford.edu  
Quality: Phrap Quality >=40 99.9% of Sequence;  
Estimated Total Number of Errors is 0.3.  
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QY	1021	GCCCGCTGTGGCTTAGAGGCTCCCTCTGTGAGGGAGCAGCCCTCCCCAGATAACCT	1080	
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QY 1141 CCGCAGCTTCCTGGCACTACCTGAGCCGGAGACCCAGGACTGGCGCGCCATGCCGC 1200
Db 147756 CCGCAGCTTCCTGGCACTACCTGAGCCGGAGACCCAGGACTGGCGCGCCATGCCGC 147697

QY 1201 AGTAGGTTCTAGGGGGCGGTGCTGCTGCTGCTGCCAGTGGACTGGCCCTGCAGGTGAGCACTGCC 1260
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QY 1501 GTCCTCTCTGAGCCTTGGTTTCTTCAGCAGTGAGATGCTCAGATAAATGCTGTCTCCCA 1560
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QY 1561 TGATGGTGTGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGGGTGTG 1620
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QY 1801 GCTCATTT 1808
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RESULT 12
AX179291
LOCUS AX179291 1153 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 4 from Patent WO014446.
ACCESSION AX179291
VERSION AX179291.1 GI:14598961
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL 21612, 21615, 21620, 21676, 33756, novel human alcohol
dehydrogenases
Patent: WO 014446-A 4 21-JUN-2001;
Millennium Pharmaceuticals, Inc. (US)
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source Location/Qualifiers
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Best Local Similarity 99.8%; Pred. No. 3.2e-163;
Matches 918; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 264 AGGAGGCAACATCATCTTGGCTGCCGAGACATGGAGAACTGTGAGCGGCAGCAAAGGA 323
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QY 324 CATCCGCGGGAGACCTCAATCAATCAATGTCAACGCCCGGCACCTTGGCTTCCCT 383
Db 294 CATCCGCGGGAGACCTCAATCAATCAATGTCAACGCCCGGCACCTTGGCTTCCCT 353

QY 384 CAAGTCTATCCGAGAGTTTGCAGCAAAGATCATTTGAAGAGGAGCGAGTGGACATTCT 443
Db 354 CAAGTCTATCCGAGAGTTTGCAGCAAAGATCATTTGAAGAGGAGCGAGTGGACATTCT 413

QY 444 AATCAACAACCGCGGTGTGATGCGGTGCCCTCCCTCACTGGACCAACCGAGGACGGCTTCGAGAT 503
Db 414 AATCAACAACCGCGGTGTGATGCGGTGCCCTCCCTCACTGGACCAACCGAGGACGGCTTCGAGAT 473

QY 504 GCAGTTTGGCGTTAACCACTGGGTCACTTTCTTGTGACAAACTTGTGCTGGACAAGCT 563
Db 474 GCAGTTTGGCGTTAACCACTGGGTCACTTTCTTGTGACAAACTTGTGCTGGACAAGCT 533

QY 564 GAAAGCCTCAGCCCTTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGGGCA 623
Db 534 GAAAGCCTCAGCCCTTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGGGCA 593

QY 624 CATAGACTTTGACGACTTGAACCTGGCAGACGAGGAAGTATAACAAAGCCGCTACTG 683
Db 594 CATAGACTTTGACGACTTGAACCTGGCAGACGAGGAAGTATAACAAAGCCGCTACTG 653

QY 684 CCAGAGCAAGCTCGCCCATCGTCTCTTCAACCAAGGAGCTGAGCCGGCGGTGCAAGGCTC 743
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QY 744 TGGTGTGACTGTCAACGCCCTGCACCCCGCGCTGGCCAGGACAGAGCTGGGCAGACAC 803
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QY 804 GGGCATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCCATCTTCTGGCTGCTGGT 863
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QY 864 CAAGAGCCCGAGTGGCCGCCAGCCAGCAGCAGCATATACTGGCCGTGGCGGAGGAACCTGGC 923
Db 834 CAAGAGCCCGAGTGGCCGCCAGCCAGCAGCAGCATATACTGGCCGTGGCGGAGGAACCTGGC 893

QY 924 GGATGTTTCCGAAAGTACTTTCGATGGACTCAAAAGGAGCCCGGCCCGAGGCTGA 983
Db 894 GGATGTTTCCGAAAGTACTTTCGATGGACTCAAAAGGAGCCCGGCCCGAGGCTGA 953

QY 984 GGATGAGGAGTGGCCCGGAGGCTTTGGGCTGAAAGTGCCTGGCTTGGGCTTAGAGGC 1043
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QY 1044 TCCCTCTGTGAGGAGCAGCCCTTCCAGATACCTCTGGAGCAGATTGAAAGCCAGG 1103
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RESULT 13

AX136638/c

LOCUS AX136638 554 bp DNA linear PAT 30-MAY-2001

DEFINITION Sequence 560 from Patent EP1067182.

ACCESSION AX136638

VERSION AX136638.1 GI:14273042

KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)

REFERENCE

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.

TITLE Secretory protein or membrane protein

JOURNAL Patent: EP 1067182-A 560 10-JAN-2001; Helix Research Institute (JP)

FEATURES

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Best Local Similarity 96.9%; Pred. No. 2.3e-84;

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Db 554 ACTGCCTTGNTTCTGGCTGGTTCCGTCCTGCTGTTGCTGCCAGCA--GGAAAAGGNCCATC 497

QY 1313 TGATGCTTCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTCTGTGCACT 1372

Db 496 TGATGCTTCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTCCACGCAC 437

QY 1373 TGCAGGCCACGTTCAGGAGAGCCAGCGGTGCCCTGTTCGGGAGGGTTCCAGGTCTCCGTG 1432

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QY 1433 AAGAGCATGGGCAAGTTGTC-TGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCTTGT 1491

Db 377 AAGAGCATGGGCAAGTTGTC-TGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCTTGT 318

QY 1492 GCATGCATGGTCCCTCTGAGCCTTGGTTTTCAGCAGTGAGATGCTCAGAATAACTGC 1551

Db 317 GCATGCATGGTCCCTCTGAGCCTTGGTTTTCAGCAGTGAGATGCTCAGAATAACTGC 258

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Db 257 TGTCTCCCATGATGGTGGTACAGCGAGCTGTGCTTGGGTCCCTGTGGGACCTTGT 198

QY 1612 GGGTGTCTGAGGGCTTCCCTGTGCCAGAGCCAGAGAGCAGGAGCAGGTGTCAGTGTGAT 1671

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QY 1672 CCGAGTTCAGGCTCTGCAGCGCATGGAGTGGGAACCCACCAGCTGTGCTACAGGACC 1731

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QY 1732 TGGGATGCTGGGACTCCACCTTCCCTATCAATTCTCATGGTAGTCCAAACTGCAGACT 1791

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QY 1792 CTCAAACTTGTCTCATTT 1808

Db 17 CTCAAACTTGTCTCATTT 1

RESULT 14

BD123878/c

LOCUS BD123878 554 bp DNA linear PAT 18-SEP-2002

DEFINITION Secretory protein or membrane protein.

ACCESSION BD123878

VERSION BD123878.1 GI:23218823

KEYWORDS JP 2002017376-A/387.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.

TITLE Secretory protein or membrane protein

JOURNAL Patent: JP 2002017376-A 387 22-JAN-2002; HELIX RESEARCH INSTITUTE

COMMENT

OS Homo sapiens (human)

PN JP 2002017376-A/387

PD 22-JAN-2002

PF 07-JUL-2000 JP 2000253173

PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,TOMOYASU SUGIYAMA,

PI KOJI HAYASHI

PC

C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC 10,

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Secretory protein or membrane protein

FH Key Location/Qualifiers

FT source 1. .554

FT /organism="Homo sapiens (human)"

FEATURES

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Best Local Similarity 96.9%; Pred. No. 2.3e-84;

Matches 540; Conservative 0; Mismatches 13; Indels 4; Gaps 3;

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Db 554 ACTGCCTTGNTTCTGGCTGGTTCCGTCCTGCTGTTGCTGCCAGCA--GGAAAAGGNCCATC 497

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Db	137	CCTGAGTTTCAGGCTCTGCACGGGCATGGAGTGGGAACCCACCAGCTGCTGCTACAGGACC	78
QY	1732	TGGGATTGCCTGGGACTCCACACCTTCCTATCAATTCTCATGGTAGTCCAAACTGCAGACT	1791
Db	77	TGGGATTGCCTGGGACTCCACACCTTCCTATCAATTCTCATGGTAGTCCAAACTGCAGACT	18
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RESULT 15
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DEFINITION      Sequence 437 from Patent WO2222660.
ACCESSION      AX406022
VERSION      AX406022.1      GI:21439483
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    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1
AUTHORS      Tang,Y.T., Liu,C., Zhou,P., Asundi,V., Zhang,J., Zhao,Q.A., Ren,F.,
      Xue,A.J., Yang,Y., Wehrman,T. and Drmanac,R.T.
TITLE      Novel nucleic acids and polypeptides
JOURNAL      Patent: WO 0222660-A 437 21-MAR-2002;
      HYSEQ, INC. (US)
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QY	61	GACGCTGTCCCCGGCCCGGCATGAGCGGCTACCTGTCGCGCTGTCCGCGCTGGGCACG	120		
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QY	121	GTAGCAGCGCGCCGCTGCTGCTCAAGGACTATGTACCGGTGGGGCTTGCCCGAGCAAG	180		
Db	128	GTAGCAGCGCGCCGCTGCTGCTCAAGGACTATGTACCGGTGGGGCTTGCCCGAGCAAG	187		
QY	181	GCCACCATCCCTGGGAAGACGGTTCATCTGTACGGGCGGCCAACACAGGCATCGGGAAGCAG	240		
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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23: em\_gss\_mus:\*  
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25: em\_gss\_rod:\*  
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28: gb\_gssl:\*  
29: gb\_gss2:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	885.4	49.0	896	BX393531	BX393531
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6	791.4	43.8	882	12	AGENCOURT	AGENCOURT
7	777	43.0	1136	12	AGENCOURT	AGENCOURT
8	769	42.5	892	13	AGENCOURT	AGENCOURT
9	749.2	41.4	892	13	AGENCOURT	AGENCOURT
10	740.4	41.0	933	13	AGENCOURT	AGENCOURT
11	727.8	40.3	1019	12	AGENCOURT	AGENCOURT
12	726	40.2	2696	11	AGENCOURT	AGENCOURT
13	724	40.0	756	10	AGENCOURT	AGENCOURT
14	722.4	40.0	734	12	AGENCOURT	AGENCOURT
15	721	39.9	831	12	AGENCOURT	AGENCOURT
16	718.2	39.7	791	14	AGENCOURT	AGENCOURT
17	715.6	39.6	1036	12	AGENCOURT	AGENCOURT
18	709.4	39.2	940	13	AGENCOURT	AGENCOURT
19	703.2	38.9	1073	12	AGENCOURT	AGENCOURT
20	699	38.7	801	29	AGENCOURT	AGENCOURT
21	698	38.6	1101	10	AGENCOURT	AGENCOURT
22	695.8	38.5	937	13	AGENCOURT	AGENCOURT
23	677.4	37.5	709	9	AGENCOURT	AGENCOURT
24	672.8	37.2	694	10	AGENCOURT	AGENCOURT
25	660.6	36.5	841	10	AGENCOURT	AGENCOURT
26	649.4	35.9	875	13	AGENCOURT	AGENCOURT
27	643.2	35.6	856	13	AGENCOURT	AGENCOURT
28	642.6	35.5	753	29	AGENCOURT	AGENCOURT
29	632.2	35.0	656	14	AGENCOURT	AGENCOURT
30	625.6	34.6	712	12	AGENCOURT	AGENCOURT
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32	625	34.6	1224	10	AGENCOURT	AGENCOURT
33	619.4	34.3	646	12	AGENCOURT	AGENCOURT
34	617.2	34.1	660	9	AGENCOURT	AGENCOURT
35	616.8	34.1	913	13	AGENCOURT	AGENCOURT
36	616	34.1	1080	13	AGENCOURT	AGENCOURT
37	610.4	33.8	631	14	AGENCOURT	AGENCOURT
38	608.6	33.7	627	14	AGENCOURT	AGENCOURT
39	606.2	33.5	759	10	AGENCOURT	AGENCOURT
40	601	33.2	663	12	AGENCOURT	AGENCOURT
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44	589	32.6	597	10	AGENCOURT	AGENCOURT
45	587	32.5	589	12	AGENCOURT	AGENCOURT

ALIGNMENTS

RESULT 1  
BX393531  
LOCUS  
DEFINITION  
BX393531 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens  
CDNA clone CS0DB006Y021 5-PRIME, mRNA sequence.  
ACCESSION  
BX393531  
VERSION  
BX393531.1 GI:30627901  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
REFERENCE  
1 (bases 1 to 1201)  
AUTHORS  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE  
Full-length cDNA libraries and normalization  
JOURNAL  
Unpublished (2001)  
COMMENT  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 9526.r For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0DB006Y021&cluster=9526.r. Contact :  
Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600





QY 472 CCCCACTGGACACCGAGGACGGCTTCGAGATGCAGTTTGGCGTTAACCACTGGGTGAC 531  
Db |||||  
61 CCCCACTGGACACCGAGGACGGCTTCGAGATGCAGTTTGGCGTTAACCACTGGGTGAC 120  
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181 AACCTCTCGTCCCTGGCCCCATGTTGCTGGGCACATAGACTTTGACGACTTGAACTGGCAG 240  
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Db |||||  
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QY 892 AGCACATACCTGGCGGCGGAGGAACTGGCGGATGTTTCCGAAAGTACTTCGATGGA 951  
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721 CCGCCATGCCCGCAGCTTCTTGCCACTACCTGAGCCGGAGACCCAGGACTGGCGGCCGC 780  
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Db |||||  
781 CATGCCCGCAGTAGTTCAGGGGGCGGTGCTGCGCCGAGTGACTGGCCTGCAGGTGAG 840  
QY 1252 CACTGCCCGGGCTCTGGCTGGTTCCGTCTGCTGCTGCCAGCAGGGGAGAGGGG 1307  
Db |||||  
841 CACTGCCCTGGGCTCGGGCTGGTTCCGTCTGCTGCTGCCANCAAGGGAGAGGG 896

RESULT 3  
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LOCUS  
DEFINITION BQ682452 982 bp mRNA linear EST 15-JUL-2002  
AGENCOURT\_8034326 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:6213843  
5', mRNA sequence.  
ACCESSION BQ682452  
VERSION BQ682452.1 GI:21795131  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 982)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)

COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: DCTD/Drp  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM2380 row: d column: 04  
High quality sequence stop: 717.  
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

ORIGIN

Query Match 47.0%; Score 849; DB 13; Length 982;  
Best Local Similarity 96.9%; Pred. No. 1e-157;  
Matches 887; Conservative 0; Mismatches 25; Indels 3; Gaps 2;  
QY 4 CTACCCAGGGCGCTGTGTGCAGCAAGCTCCGGCCCGACTCCGGACGCGCTGACGCGCTGAC 63  
Db |||||  
1 CTACCCAGGGCGCTGTGTGCAGCAAGCTCCGGCCCGACCCCGGACGCGCTGACGCGCTGAC 60  
QY 64 GCCTGTCCCCGGCCCGGCATGAGCCGCTACCTGTGCGCGCTGTGCGCGCTGGGCACGGTA 123  
Db |||||  
61 GCCTGTCCCCGGCCCGGCATGAGCCGCTACCTGTGCGCGCTGTGCGCGCTGGGCACGGTA 120  
QY 124 GCAGGCGCGCCGCTGTGCTCAAGGACTATGTACCGGTGGGCTTGCCCCCAGCAAGGCC 183  
Db |||||  
121 GCAGGCGCGCCGCTGTGCTCAAGGACTATGTACCGGTGGGCTTGCCCCCAGCAAGGCC 180  
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Db |||||  
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QY 424 GAGGAGCGAGTGGACATTCCTAATCAACACCGCGGGTGTGATGCGGTGCCCCCAGTGAGCC 483  
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481 ACCGAGGACGGCTTCGAGATGCAGTTTGGCGTTTAAACACCTGGGTGCTTCTCTTGACA 540  
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QY 664 AACACCAAAAGCCGCTACTGCCAGAGCAAGCTCGCCATCGTCTCTTCCACCAAGGAGCTG 723
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QY 901 CTGGCCGTGGCGGAG 915
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LOCUS
DEFINITION BQ682333 935 bp mRNA linear EST 15-JUL-2002
5', mRNA sequence.
AGENCY BQ682333.1 GI:21795012
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 935)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-roman@nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2432 row: 1 column: 08
High quality sequence stop: 657.
Location/Qualifiers
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/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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FEATURES

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/clone="IMAGE:6265495"
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/lab_host="DH10B (phage-resistant)"
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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ORIGIN

Query Match 45.8%; Score 828.6; DB 13; Length 935;

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Best Local Similarity 98.5%; Pred. No. 1.1e-153;
Matches 857; Conservative 0; Mismatches 10; Indels 3; Gaps 2;
QY 323 ACATCCGCGGGAGACCCCTCAATCACCATTGTAACGCCCGGCACCTGGACTTGGCTTCCC 382
Db 1 ACATCCGCGGGAGACCCCTCAATCACCATTGTAACGCCCGGCACCTGGACTTGGCTTCCC 60
QY 383 TCAAGTCTATCCGAGAGTTTGCAGCAAAAGATCATTTGAAGAGGAGGAGCGAGTGGACATTC 442
Db 61 TCAAGTCTATCCGAGAGTTTGCAGCAAAAGATCATTTGAAGAGGAGGAGCGAGTGGACATTC 120
QY 443 TAATCAACAAACGCGGTGTGATCGCGTGCCTCCCACTGGACCACCGAGGACGCGCTTCGAGA 502
Db 121 TAATCAACAAACGCGGTGTGATCGCGTGCCTCCCACTGGACCACCGAGGACGCGCTTCGAGA 180
QY 503 TGCAGTTTGGCGTTAACCACTGGGTCACTTTCTTTGACAAACTTGTCTGCTGGACAAGC 562
Db 181 TGCAGTTTGGCGTTAACCACTGGGTCACTTTCTTTGACAAACTTGTCTGCTGGACAAGC 240
QY 563 TGAAGCGCTCAGCCCCCTTCGCGGATCATCAACCTCTGTCCTTGGCCCATGTTGCTGGGC 622
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QY 623 ACATAGACTTTGACGACTTGAATGCGCAGACGAGGAAGTATAACACCAAAAGCCGCTACT 682
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QY 683 GCCAGAGCAAGCTCGCCATCGTCTCTTCAACCAAGGAGCTGAGCCGCGGCTGCAAGGCT 742
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QY 743 CTGGTGTGACTGTCAACGCCCTTGACCCCGGCGTGGCCAGGACAGAGCTGGGCAGACACA 802
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QY 803 CGGGCATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCCATCTTCTGGCTGCTGG 862
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QY 1043 CTCCTCTGTGAGGAGCAGCCCTCTCCAGATACCTCTGGAGCAGATTTGAAAGCCAG 1102
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QY 1103 GATGGCGCCT-CCAGACCGAGGACAGCTGTCCGCCCATGCCCGCAGCTTCTGCGCACTACC 1161
Db 781 GATGGCGCCTCCAGACCGAGGACCGCTGTCCGCCCATGCCCGCAGCTTCTGCGCACTACC 840
QY 1162 TGAGCC--GGGAGACCCAGGACTGGCGGCC 1189
Db 841 TGAACCCGGGAAGACCCAGGACTGGGGGGC 870
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RESULT 5  
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LOCUS  
DEFINITION BQ6810961 1063 bp mRNA linear EST 05-MAR-2002  
5', mRNA sequence.  
AGENCY BQ6810961.1 GI:19127784  
KEYWORDS EST.  
SOURCE Homo sapiens (human)



ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1063)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: DCTD/DTP  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM1984 row: m column: 10  
High quality sequence stop: 602.  
Location/Qualifiers  
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

Query Match 44.2%; Score 799; DB 12; Length 1063;  
Best Local Similarity 95.6%; Pred. No. 8.7e-148;  
Matches 853; Conservative 0; Mismatches 36; Indels 3; Gaps 3;

QY 726 CCGGCGGCTGAAGGCTCTGGTGTGACTGTCAACGCCCTGCACCCCGCGTGGCCAGGAC 785  
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QY 786 AGAGCTGGGCAGACACACGGGCATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCC 845  
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QY 846 CATCTTCTGGCTGCTGGTCAAGAGCCCGAGCTGGCCGCCAGCCAGCCAGCATACCTGGC 905  
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QY 906 CGTGGCGGAGAACTGGCGGATGTTTCGGGAAAGTACTTCGATGGACTCAACACAGAGGC 965  
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QY 1026 CCTGGTGGCTTAGAGGCTCCCTCTGTGAGGGAGCAGCCCTCCAGATACCTCTGGA 1085  
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QY 1086 GCAGATTGAAAGCCAGGATGGCGCTCCAGCCGAGGACAGCTGTCCGCCATGCCCGCA 1145  
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QY 1146 GCTTCCTGGCACTACCTGAGCCGGGAGACCAGGACTGGCGGCGCGCATGCCCGCAGTAG 1205  
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QY 1505 TCTCTG-AGCCTTGGTTTCTTTCAGCAGTGTGCTGTGGCTATGGCATGGTGTGCCGGGG 1562  
Db 781 TCTCTGAACCCCTGGTTTCTTTCAGCAGGGAATGCTCAGAATAACTGGCTGTCTCCCTG 840

QY 1563 ATGGTGTGTACAGCGAGCTGTGTCTGTGGCTATGGCATGGTGTGCCGGGG 1614  
Db 841 AAGGGGTGGGACCACCGAAGCTGTGTGGCTATGGGTATGGGCTGGCCTGGGG 892

RESULT 6  
BG822129 882 bp mRNA linear EST 22-MAY-2001  
LOCUS 602726271F1 NIH\_MGC\_15 Homo sapiens cDNA clone IMAGE:4865873 5',  
DEFINITION mRNA sequence.

ACCESSION  
BG822129  
VERSION BG822129.1 GI:14169716  
KEYWORDS EST.

SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1 (bases 1 to 882)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: NIH Intramural Sequencing Center  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
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Location/Qualifiers

1. .882  
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/note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)"

FEATURES  
source

VERSION BM914938.1 GI:19365317  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 1136)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: DCTD/DTF  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
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 EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
 into EcoRI/XhoI sites using the following 5' adaptor:  
 GGCACCAG(G). Library constructed by Ling Hong in the  
 laboratory of Gerald M. Rubin (University of California,  
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
 Superscript II RT (Life Technologies). Note: this is a  
 NIH\_MGC Library."  
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 Best Local Similarity 95.0%; Pred. No. 2.1e-143;  
 Matches 814; Conservative 0; Mismatches 40; Indels 3; Gaps 1;  
 QY 718 GAGCTGAGCCGGCGCTGCAAGGCTCTGGTGTGACTGTCAACGCCCTGCACCCCGCGGTG 777  
 Db 16 GACGAGGGCGCGGCTGCAAGTCTCTGGTGTGACTGTCAACGCCCTGCACCCCGCGGTG 75  
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 QY 1078 CCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAGACCGAGGACAGCTGTCCGCCA 1137  
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ORIGIN		Query Match	Score	DB	Length
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		Indels	6;	Gaps	5;
QY	23	GCAGCAAGCTCCGGCCGACTCCGGACGCCCTGACGCTGACGCCTGTCCCGGCCCGGCA	82		
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QY	83	TGAGCCGCTACCTGTGCTCCGCTGTTCGGCGTGGCAGCGGTAGCAGGCGCGCTGTCTGC	142		
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QY	143	TCAAGGACTATGTCAACCGTGGGCTTGCCCGCAGCAAGGCCACCATCCCTGGGAAGACGG	202		
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QY	263	GAGGAGCAACATCATCTCTGGCCTGCCGAGACATGGAGAAGTGTGAGGCGGCACCAAGG	322		
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QY	323	ACATCCGGGGGAGACCCCTCAATCACCATGTCAACGCCCGGCACCTGGACTTGGCTTCCC	382		
DB	302	ACATCCGGGGGAGACCCCTCAATCACCATGTCAACGCCCGGCACCTGGACTTGGCTTCCC	361		
QY	383	TCAAGTCTATCCGAGAGTTGCAGCAAAAGATCATTTAA - GAGGAGGAGCGAGTGGACATT	441		
DB	362	TCAAGTCTATCCGAGAGTTGCAGCAAAAGATCATTTAA - GAGGAGGAGCGAGTGGACATT	421		
QY	442	CTAATCAACAAACGGGGTGTGATCGGGTCCCCCACTCGACCAACCGAGGACGGCTTCGAG	501		
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QY	502	ATGCAGTTTGGCGTTAACACACCTGGGTCACTTTCTTTGACAAAATTGCTGTGGAACAAG	561		
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QY	562	CTGAAAGCCTCAGCCCTTCGCGGA - TCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG	620		
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DB	662	CTGCCAGAGCAAGCTCGCCATCGTCTCTTCAACCAAGGAGCTGAGCCGGCGGCTTGCAAG	721		
QY	740	GCTCTGGTGTGACTGTCAACGCGCTGCACCCCGCGTGGCCAGGACAGAGCTGGGCAGAC	799		
DB	722	GCTCTGGTGTGACTGTCAACGCGCTGCACCCCGCGTGGCCAGGACAGAGCTGGGCAGAC	781		
QY	800	ACAC - GGGCATCCATGGCTCCACCTTCTCCAGCAC - ACATCGGGCCCATCTTCTGSC	856		
DB	782	ACACGGGGCATCCATGGGTCCACCTTCTCAGGCACCAAAATTGGGACCATCTTCTGSC	841		
QY	857	TGCTGGTCAAGAGCCCGAGCTGGCCGCCAGCCCGAGCA	895		
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BM914938					
LOCUS					
DEFINITION					
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QY 1378 GCCACGTGAGGAGGCCAGCGGTGCCTGTGCGGGAGGGTTCCAAGGTGCTCCGTGAAGAG 1437  
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DEFINITION BU931992 892 bp mRNA linear EST 18-OCT-2002  
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IMAGE:6672291 5', mRNA\_sequence.  
ACCESSION BU931992  
VERSION BU931992.1 GI:24120811  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 892)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contract: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
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XhoI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCACGAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

ORIGIN

Query Match 42.5%; Score 769; DB 13; Length 892;  
Best Local Similarity 96.2%; Pred. No. 7.le-142;  
Matches 852; Conservative 0; Mismatches 23; Indels 11; Gaps 6;

QY 160 GGTGGGGCTTGCCCCAGCAAGGCCACCATCCCTTGGGAAGACGGTTCATCTGACGGGCGCC 219  
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QY 220 AACACAGGCATCGGGAAGCAGACCGCCTTGGAACTGGCCAGGAGAGGAGGCAACATCATC 279  
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QY 280 CTGGCCTGCCGAGACATGGAGAAAGTGTGAGGCGGCAGCAAAGGACATCCGCGGGGAGACC 339  
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QY 880 GCCGCCAGCCAGCACATACCTGGCC--GTGGCGGAGGAAGTGGCGGATGTTT-CCGG 935  
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QY 936 AAAGTACTT-CGATGGACTCAAAACAG-AAGGCCCGGCCCGGAGGCTGA--GGATGAGG 991  
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LOCUS BU168826 892 bp mRNA linear EST 04-SEP-2002  
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ACCESSION BU168826  
VERSION BU168826.1 GI:22682810  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 892)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-re@mail.nih.gov](mailto:cgapbs-re@mail.nih.gov)  
Tissue Procurement: DCTD/DTP  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
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<http://image.llnl.gov>  
Plate: LLCM2399 row: p column: 11  
High quality sequence stop: 641.  
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EcoRI; CDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G). Library constructed by Ling Hong in the  
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Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."  
ORIGIN  
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VERSION BU190625.1 GI:22704609  
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ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 933)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-re@mail.nih.gov](mailto:cgapbs-re@mail.nih.gov)  
Tissue Procurement: DCTD/DTP  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM2359 row: c column: 18  
High quality sequence stop: 656.  
FEATURES  
source  
1..933  
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 41.0%; Score 740.4; DB 13; Length 933;  
Best Local Similarity 97.7%; Pred. No. 3.4e-136;  
Matches 762; Conservative 0; Mismatches 16; Indels 2; Gaps 1;  
  
QY 4 CTACCCAGGCGGTGTGTCAGCAAGCTCCGCGCGACTCCGGACGCTGACGCTGAC 63  
Db 1 CTACCCAGGCGGTGTGTCAGCAAGCTCCGCGCGACTCCGGACGCTGACGCTGAC 60  
  
QY 64 GCCTGTCCCGCGCGCATGAGCCGCTACCTGTGCCGTGTCCGCGTGGCGACGGTA 123  
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Db 601 CTGGCCCATGTTGCTGGGCACATAGACTTTGACGACTTGAACCTGGCAGACGAGGAAGTAT 660  
  
QY 664 AACACCAAGCCGCTACTGCCAGAGCAAGCTCGCCATCGTCTCTTCAACCAAGGAGCTG 723  
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QY 724 AGCCGGCGGCTGCAA--GGCTCTGGTGTGACTGTCAACGCCCTGCACCCCGCGGTGGCCA 781  
Db 721 AGCCGGCGGCTGCAAAGGCTCCTGGTGTGACTGTCAACGCCCTGGCACCCCGCGGTGGCA 780

RESULT 11  
B1117371  
LOCUS  
DEFINITION B1117371 NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:5016556 5',  
mRNA sequence.  
ACCESSION B1117371  
VERSION B1117371.1 GI:14568272

KEYWORDS

SOURCE  
ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1019)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCMI827 row: e column: 05

High quality sequence stop: 755.

FEATURES

Location/Qualifiers

1..1019

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/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5016556"

/tissue\_type="small cell carcinoma"

/cell\_line="MGC3"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_7"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 40.3%; Score 727.8; DB 12; Length 1019;

Best Local Similarity 92.7%; Pred. No. 1.1e-133;

Matches 895; Conservative 0; Mismatches 57; Indels 13; Gaps 12;

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QY 794 GCAGACACACGGGCATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCCATCTTCT 853  
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Db 421 GCACTACCTGAGCGGGAGACCCAGGACTGCGGGCCGCCATGCGCGCAGTAGGTTCTAGG 480

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Db 541 TTCGGTCTGCTCTGCTGCCAGCAGGGGAGCAGGGGCCATCTGATGCTTCCCCTGGGAATC 600

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QY 1507 TCTGAGCCTTGGTTCTTTCAGCAGTGAGATGCTCAGAATACTGTGTCTCTCCCATGA-TG 1565

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QY 1566 GTGTGGTACAGCG-AGCTGTTGTCTGGCTATGGCATGGCTGTG-CCGGGGGTGTTTGTCTG 1623

Db 840 GTGTGGTACAGCGAAGCTGTTGTCTGGCTATGGCATGCTTGTGCCCGGGGTGTTTGCCA 899

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QY 1684 CTCTG 1688

Db 960 CACGG 964

RESULT 12

AK028434

LOCUS

DEFINITION Mus musculus 14 days embryo liver cDNA, RIKEN full-length enriched library, clone:4432411I09 product:weakly similar to SD07613P [Drosophila melanogaster], full insert sequence.

ACCESSION AK028434

VERSION AK028434.1 GI:26324391

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wataniki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

CDS

Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861

4  
The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

5  
The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)

6 (bases 1 to 2696)  
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bonc,H., Carninci,P.,  
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,  
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,  
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,  
Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,  
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,  
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,  
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,  
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,  
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,  
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,  
Muramatsu,M. and Hayashizaki,Y.  
Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail:genome-res@gs.riken.go.jp,  
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,  
Fax:81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.

URL:http://genome.gsc.riken.go.jp/  
URL:http://fantom.gsc.riken.go.jp/.

Location/Qualifiers  
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polyA_site		2696		/note="putative"	
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Query Match 40.2%; Score 726; DB 11; Length 2696;					
Best Local Similarity 82.2%; Pred. No. 4e-133;					
Matches 850; Conservative 0; Mismatches 175; Indels 9; Gaps 1;					
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QY	122	TAGCAGGCGCCGCGTGTCTCAAGGACTATGTACCGGTGGGCTTGCCCGCAGCAAG	181		
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QY	542	CAAACTTGCTGTGGACAAAGCTGAAGCCCTCAGCCCTTCGCGGATCATCAACCTCTCGT	601		
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QY	782	GGACAGAGCTGGGCAGACACACGGGCATCCATGGCTCCACCTTCTCCAGCACCACTCG	841		
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QY	842	GGCCCATCTTCTGGCTGCTGTTCAAGAGCCCGAGCTGGCGCCCGCCAGCCACATACC	901		
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QY	962	AGGCCCGGCCCCGAGGCTGAGGATGAGGAGTGGCCCCGAGGCTTTGGGCTGAAAGTG	1021		
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QY	1022	CCCGCCTGGTGGGCTTAG-----AGGCTCCCTCTGTGAGGGAGCAGCCCTCCCA	1079		
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RESULT 13					
BE559808					
LOCUS					
DEFINITION	BE559808 601346972F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687808 5', mRNA sequence.				
ACCESSION	BE559808				
VERSION	BE559808.1 GI:9803527				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
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REFERENCE	1 (bases 1 to 756)				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLM379 row: p column: 17 High quality sequence stop: 753.				
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	/lab_host="DH10B (phage-resistant)"				
	/clone_lib="NIH_MGC_8"				
	/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."				
ORIGIN					
Query Match 40.0%; Score 724; DB 10; Length 756;					
Best Local Similarity 99.1%; Pred. No. 5.5e-133;					
Matches 749; Conservative 0; Mismatches 5; Indels 2; Gaps 2					
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QY	61	GACGCTGTCCCGCCGCGCATGAGCCGCTACCTGCTGCCGTGTGCGGCTGGGCACG	120		
Db	61	GACGCTGTCCCGCCGCGCATGAGCCGCTACCTGCTGCCGTGTGCGGCTGGGCACG	120		
QY	121	GACGAGGCGCCCGCTGCTGCTCAAGGACTATGTACCGGTGGGCTTGCCCCAGCAAG	180		
Db	121	GACGAGGCGCCCGCTGCTGCTCAAGGACTATGTACCGGTGGGCTTGCCCCAGCAAG	180		
QY	181	GCCACCATCCCTGGGAGACGGTTCATCGTGACGGGCGCCCAACACAGGCATCGGAACGAG	240		

QY	1022	CCCGCCTGGTGGCTTAG-----AGGCTCCCTCTGTGAGGGAGCAGCCCTCCCCA	1072	
Db	1080	CCCGTTTGGTGGCTTGGCCATGGCTCATGGATCCCTGGGAGAGGACATGCCATTCCCA	1139	
QY	1073	GATAACCTCTGGAG	1086	
Db	1140	GATAACCTTCAGAG	1153	
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BE559808				
LOCUS				
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VERSION	BE559808.1	GI:9803527		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 756)			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs@mail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cdna Library Preparation: Ling Hong/Rubin Laboratory cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LCM379 row: p column: 17 High quality sequence stop: 753.			
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ORIGIN				
Query Match 40.0%; Score 724; DB 10; Length 756;				
Best Local Similarity 99.1%; Pred. No. 5.5e-133;				
Matches 749; Conservative 0; Mismatches 5; Indels 2; Gaps 2;				
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Db 661 GTATAACACCAAGCCGCTACTGTACAGCAAGCTCGCCATCGTCTCTTACCACCAAGGA 720
QY 720 GCTGAGCCGGCGGTGCAAGGCTCTGTTGTGACTGT 755
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RESULT 14

BM723409  
LOCUS BM723409 734 bp mRNA linear EST 01-MAR-2002  
DEFINITION UI-E-EJ0-aio-b-02-0-UI.r1 UI-E-EJ0 Homo sapiens cDNA clone  
UI-E-EJ0-aio-b-02-0-UI 5', mRNA sequence.

ACCESSION BM723409

VERSION BM723409.1 GI:19044666

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 734)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene

discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa

DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com).

Seq primer: M13 Reverse.

Location/Qualifiers

source

1. .734  
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/clone="UI-E-EJ0-aio-b-02-0-UI"  
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optic nerve, retina, Retina Foveal and Macular, RPE and  
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/dev\_stage="fetal and adult"  
/lab\_host="PHIOB (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-E-EJ0"  
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a  
modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
UI-E-EJ0 is a subcloned cDNA library constructed  
according to Bonaldo, Lennon and Soares, Genome Research,  
6:791-806, 1996. First strand cDNA synthesis was primed  
with an oligo-dT primer containing a Not I site. Double  
stranded cDNA was ligated to an EcoR I adaptor, digested  
with Not I, and cloned directionally into pT73-Pac  
vector. The oligonucleotide used to prime the synthesis of  
first-strand cDNA contains a library tag sequence that is  
located between the Not I site and the (dT)18 tail. The  
sequence tags for this library are: fetal eyes,  
AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment,  
AATGCCGAT; optic nerve, CCATTAGTG; retina, CCGCG; Retina  
Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This  
library was created for the program, Gene Discovery in the  
Visual System, supported by National Eye Institute (NEI)."

ORIGIN

Query Match 40.0%; Score 722.4; DB 12; Length 734;  
Best Local Similarity 99.7%; Pred. No. 1.1e-132;  
Matches 723; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 691 AAGCTCGCCATCTGCTCTTTTACCAAGAGAGCTGAGCCGGGGCTGCAAGGCTCTGGTGTG 750
Db 241 AAGCTCGCCATCTGCTCTTTTACCAAGAGAGCTGAGCCGGGGCTGCAAGGCTCTGGTGTG 300
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Db 301 ACTGTCAACGCCCTGCACCCCGCGTGGCCAGGACAGAGCTGGGCAGACACACGCGGCATC 360
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Db 361 CATGGCTCCACCTTCTCCAGCACCACTCTGGGCCCCATCTTCTGGCTGCTGGTCAAGAGC 420
QY 871 CCCGAGCTGGCCGCCAGCCCGAGCACATACCTGGCCCGTGGCGGAGGAACCTGGCGGATGTT 930
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Db 481 TCCGGAAGTACTTCGATGGACTCAAAACAGAGAGGCCCGGCCCGGAGGTGAGGATGAG 540
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RESULT 15  
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DEFINITION mRNA sequence.  
ACCESSION BI827579 831 bp mRNA linear EST 04-OCT-2001  
VERSION BI827579.1 GI:15939116  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 831)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapsb@mail.nih.gov](mailto:cgapsb@mail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM1411 row: i column: 11  
High quality sequence stop: 804.  
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1. .831  
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/note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site 2: EcoRV (destroyed); RNA source normal medulla from  
anonymous male age 27. Library is oligo-dT primed and  
directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.3 kb, insert size range  
0.9-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 013. Note:  
this is a NIH\_MGC Library."

FEATURES  
source

ORIGIN

Query Match 39.9%; Score 721; DB 12; Length 831;  
Best Local Similarity 98.1%; Pred. No. 2.2e-132;  
Matches 774; Conservative 0; Mismatches 5; Indels 10; Gaps 4;  
  
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QY 54 GACGCCTGACGCCTGTCCCGGCGCCGCGCATGAGCGCTACCTGTGCGCGCTGTGCGCGCT 113  
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Db 162 GGGCACGGTAGCAGGCGCCCGCTGCTCTCAAGGACTATGTCAACGGTGGGGTGGCCC 221  
  
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Db 222 CAGCAAGGCCACCATCCCTGGGAAGACGGTCACTCGTGACGGGCGCCAAACACAGGCATCGG 281  
  
QY 234 GAAGCAGACCGCCTTGGAACCTGGCCAGGAGGAGGAGGAAACATCATCTTGGCCTGCCGAGA 293  
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Db 282 GAAGCAGACCGCCTTGGAACCTGGCCAGGAGGAGGAGGAGGAAACATCATCTTGGCCTGCCGAGA 341  
  
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Db 342 CATGGAGAAGTGTGAGGCGGCGAGCAAAAGGACATCCGCGGGGAGACCTCAATCACCATGT 401  
  
QY 354 CAACGCCCGGCACCTGGACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAGAT 413  
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Job time : 4863 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2004, 11:03:04 ; Search time 60 Seconds  
(without alignments)  
1558.720 Million cell updates/sec

Title: US-10-015-393A-116  
Perfect score: 1695  
Sequence: 1 MSRYLLPLSALGTGAGAAVL.....ESARLVGLEAPSVREQLPR 331

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1695	100.0	331	4 AAB66121	Aab66121 Protein o
3	1695	100.0	331	4 AAE05174	Aae05174 Human dru
4	1695	100.0	331	6 AAE37278	Aae37278 Human gen
5	1695	100.0	331	6 ABO33614	Abo33614 Novel hum
6	1695	100.0	331	7 ABO44467	Abo44467 Human sec
7	1695	100.0	331	7 ABO33491	Abo33491 Novel hum
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9	1695	100.0	331	7 ADD70631	Add70631 Human sec
10	1695	100.0	331	7 ADD39708	Add39708 Human sec
11	1695	100.0	331	7 ADD70154	Add70154 Human sec
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14	1695	100.0	331	7 ADD38754	Add38754 Human sec
15	1695	100.0	331	7 ADD40185	Add40185 Human sec
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17	1695	100.0	331	7 ADE20018	Ade20018 Human sec
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19	1695	100.0	331	7 ADE21487	Ade21487 Human sec
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22	1688	99.6	331	4 AAB88356	Aab88356 Human mem
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24	1340	79.1	260	5 AAU76221	Aau76221 Human 337
25	1332	78.6	260	4 AAM40387	Aam40387 Human pol

26	1136	67.0	240	4 AAE01684	Aae01684 Human gen
27	1136	67.0	240	4 AAE03299	Aae03299 Human gen
28	1136	67.0	240	5 ABG63953	Abg63953 Human alb
29	1136	67.0	240	5 ABG64446	Abg64446 Human alb
30	1136	67.0	273	3 AAB57079	Aab57079 Human pro
31	1136	67.0	273	4 AAE03357	Aae03357 Human gen
32	1014	59.8	197	4 AAE01756	Aae01756 Human gen
33	947	55.9	290	4 AAM42173	Aam42173 Human pol
34	794	46.8	184	4 ABG15412	Abg15412 Novel hum
35	789.5	46.6	296	4 ABB58831	Abb58831 Drosophil
36	767.5	45.3	300	4 ABB58826	Abb58826 Drosophil
37	739.5	43.6	318	3 AAY82014	Aay82014 Human imm
38	739.5	43.6	318	3 AAB12158	Aab12158 Hydrophob
39	739.5	43.6	318	4 AAM01129	Aam01129 Human pro
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ALIGNMENTS

RESULT 1

AAY99372

ID AAY99372 standard; protein; 331 AA.

XX AC AAY99372;

XX 08-AUG-2000 (first entry)

DE Human PRO1430 (UNQ736) amino acid sequence SEQ ID NO:116.

XX KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis; transmembrane; secretion; immunoadhesion; pharmaceutical; screening.

XX OS Homo sapiens.

XX PN WC200012708-A2.

XX PD 09-MAR-2000. ✓

XX PF 01-SEP-1999; 99WO-US020111.

XX PR 01-SEP-1998; 98US-0098716P.

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PR 01-SEP-1998; 98US-0098750P.

PR 02-SEP-1998; 98US-0098803P.

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PR 09-SEP-1998; 98US-0099642P.

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PR 10-SEP-1998; 98US-0099815P.

PR 10-SEP-1998; 98US-0099816P.

PR 15-SEP-1998; 98US-0100385P.

PR 15-SEP-1998; 98US-0100388P.

PR 15-SEP-1998; 98US-0100390P.

PR 16-SEP-1998; 98US-0100584P.

PR 16-SEP-1998; 98US-0100627P.

PR 16-SEP-1998; 98US-0100661P.

PR 16-SEP-1998; 98US-0100662P.

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PR 26-OCT-1998; 98US-0105693P.  
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PR 29-OCT-1998; 98US-0106384P.  
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PR 30-OCT-1998; 98US-0106464P.  
PR 03-NOV-1998; 98US-0106856P.  
PR 03-NOV-1998; 98US-0106902P.

PR 03-NOV-1998; 98US-0106905P.  
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PR 03-NOV-1998; 98US-0106932P.  
PR 03-NOV-1998; 98US-0106934P.  
PR 10-NOV-1998; 98US-0107783P.  
PR 17-NOV-1998; 98US-0108775P.  
PR 17-NOV-1998; 98US-0108779P.  
PR 17-NOV-1998; 98US-0108787P.  
PR 17-NOV-1998; 98US-0108788P.  
PR 17-NOV-1998; 98US-0108801P.  
PR 17-NOV-1998; 98US-0108802P.  
PR 17-NOV-1998; 98US-0108806P.  
PR 17-NOV-1998; 98US-0108807P.  
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PR 17-NOV-1998; 98US-0108925P.  
PR 18-NOV-1998; 98US-0108848P.  
PR 18-NOV-1998; 98US-0108849P.  
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PR 18-NOV-1998; 98US-0108852P.  
PR 18-NOV-1998; 98US-0108858P.  
PR 18-NOV-1998; 98US-0108904P.

XX (GETH ) GENENTECH INC.

PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;

XX WPI; 2000-237871/20.

DR N-PSDB; AAA37054.

XX New mammalian DNA sequences encoding transmembrane, receptor or secreted  
PT PRO polypeptides, useful for screening of potential peptide or small  
PT molecule inhibitors of the relevant receptor/ligand interactions.

PS Claim 12; Fig 66; 773pp; English.

XX  
CC AAA37022 to AAA37144 encode the new isolated human transmembrane,  
CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The  
CC transmembrane and receptor PRO proteins can be used for screening of  
CC potential peptide or small molecule inhibitors of the relevant  
CC receptor/ligand interactions. The polypeptides and nucleotide sequences  
CC encoding then have various industrial applications, including uses as  
CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR  
CC primers and hybridisation probes used in the isolation of the PRO  
XX polypeptides from the present invention

SQ Sequence 331 AA;

Query Match 100.0%; Score 1695; DB 3; Length 331;  
Best Local Similarity 100.0%; Pred. No. 1e-165;  
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSRYLLPLSALGTVAGAAVLLKDYITGGACPSKATIPGKTVITGANTGIGKQTALELAR 60  
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Qy 61 RGGNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIIEEERVDI 120  
Db 61 RGGNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIIEEERVDI 120  
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Db 121 LINNAGVMRCPHWTTEDGFEMQFGVNHGLHFLLTNLLLDKLKASAPSRRIINLSSLAHVAG 180  
Qy 181 HIDFDDLNWQTRKYNNTKAAQCOSKLAIVLFTKELSRRLQSGVTYNALHPGVARTELGRH 240  
Db 181 HIDFDDLNWQTRKYNNTKAAQCOSKLAIVLFTKELSRRLQSGVTYNALHPGVARTELGRH 240  
Qy 241 TGIHGSTFSSTTLGPIFWLLVKSPELAAQPSSTYLAVAEELADVSGKYFDGLKQKAPAPEA 300  
Db 241 TGIHGSTFSSTTLGPIFWLLVKSPELAAQPSSTYLAVAEELADVSGKYFDGLKQKAPAPEA 300  
Qy 301 EDEEVARRLWAESARLVGLEAPSVREQPLPR 331





decreased expression of DME. Examples of such disorders include, autoimmune/inflammatory disorder such as acquired immune deficiency syndrome (AIDS), rheumatoid arthritis, osteoporosis; cell proliferative disorder such as actinic keratosis, atherosclerosis; developmental disorder such as epilepsy, anaemia; endocrine disorder such as acromegaly, cretinism, thyrotoxicosis; pancreatic disorder such as diabetes mellitus; eye disorder such as conjunctivitis, glaucoma, iritis; metabolic disorder such as Addison's disease, obesity; gastrointestinal disorder such as anorexia, dysphagia and hepatic tumours including nodular hyperplasia, adenomas and carcinomas. DME DNA is useful for creating 'knockin' humanised animals (pigs) or transgenic animals (mice or rats) to model human disease. DME DNA is also in useful is gene therapy. DME and its immunogenic fragments are useful for screening libraries of compounds in several drug screening assays

Sequence 331 AA;

FT	Protein	17. .331	
FT		/note= "Mature human secreted protein"	
XX			
PN	WO2003038038-A2.		
XX			
PD	08-MAY-2003.		
XX			
PF	24-OCT-2002; 2002WO-US033985.		
XX			
PR	26-OCT-2001; 2001US-0330629P.		
XX			
PA	(HUMA-) HUMAN GENOME SCI INC.		
XX			
PI	Rosen CA, Ruben SM, Birse CE, Komatsoulis GA, Choi GH;		
XX			
DR	WPI; 2003-430509/40.		
DR	N-PSDB; AAD56357.		
XX			
PT	New isolated nucleic acid molecule and human secreted proteins, useful		
PT	for diagnosing, preventing or treating diseases e.g. cancer,		
PT	atherosclerosis, anemia, multiple myeloma, hypertension, infections or		
PT	wounds.		
XX			
PS	Claim 11; Page 450-451; 468pp; English.		
XX			
CC	AAD56351-AAD56374 represent cDNAs corresponding to 16 human secreted		
CC	protein genes and AAE37272-AAE37295 represent the proteins they encode.		
CC	AAE37296-AAE37299 represent human secreted protein fragments. The genes		
CC	and their corresponding proteins are useful in diagnosing, preventing or		
CC	treating diseases or conditions such as hyperproliferative disorders		
CC	(e.g. cancer), immune/haematopoietic disorders (e.g. anaemia, multiple		
CC	myeloma, arthritis, asthma, acquired immune deficiency syndrome (AIDS),		
CC	rheumatoid arthritis, inflammation, psoriasis, diabetes, systemic lupus		
CC	erythematosus or allergy), reproductive system disorders (e.g. gout or		
CC	menorrhoea or epididymitis), musculoskeletal disorders (e.g. arrhythmia,		
CC	multiple sclerosis), cardiovascular disorders (e.g. arrhythmia,		
CC	congestive heart failure, hypertension or atherosclerosis), genetic		
CC	disorders (e.g. neurofibromatosis), renal disorders (e.g. urolithiasis),		
CC	neurological disorders (e.g. Alzheimer's disease or Parkinson's disease),		
CC	respiratory disorders (e.g. emphysema or bronchitis), endocrine disorders		
CC	(e.g. goitre or diabetes), digestive diseases (e.g. hepatitis),		
CC	infections or wounds. Polynucleotides of the invention may also be used		
CC	for chromosome mapping or drug screening. They are also useful in gene		
CC	therapy. The present sequence represents a human secreted protein of the		
XX	invention		
XX			
SQ	Sequence 331 AA;		

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Location/Qualifiers
1. .16
/label= Signal peptide
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Db	301	EDEVARRLWAESARLVGLEAPSVREQPLPR	331	
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ID	ABO33614 standard; protein; 331 AA.			
XX	AC	ABO33614;		
XX	DT	17-SEP-2003 (first entry)		
XX	DE	Novel human secreted and transmembrane protein PRO1430.		
XX	KW	Human; secreted and transmembrane protein; PRO; angiogenesis;		
KW	KW	endothelial cell proliferation; wound healing; immune response;		
KW	KW	T-lymphocytes proliferation; neonatal heart hypertrophy; tumour;		
KW	KW	cardiac insufficiency disorder; calcium flux; inflammation;		
KW	KW	vascular endothelial growth factor-stimulated proliferation;		
KW	KW	mammalian kidney mesangial cell proliferation; Berger disease;		
KW	KW	nephropathy; Schanlein-Henoch purpura; celiac disease; Crohn's disease;		
KW	KW	dermatitis herpetiformis; diabetes; haemoglobin switch; insulinaemia;		
KW	KW	pancreatic beta-cell precursor cell differentiation; thalassenias;		
KW	KW	obesity; auditory hair cell regeneration; hearing loss; bone disorder;		
KW	KW	cartilage disorder; sports injury; arthritis.		
XX	OS	Homo sapiens.		
XX	PN	US2003073130-A1.		
XX	PD	17-APR-2003.		
XX	PF	11-DEC-2001; 2001US-00015869.		
XX	PR	01-SEP-1998; 98US-0098716P.		
PR	PR	01-SEP-1998; 98US-0098723P.		
PR	PR	01-SEP-1998; 98US-0098749P.		
PR	PR	01-SEP-1998; 98US-0098750P.		
PR	PR	02-SEP-1998; 98US-0098803P.		
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PR	PR	02-SEP-1998; 98US-0098843P.		
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PR	PR	09-SEP-1998; 98US-0099596P.		
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PR	PR	10-SEP-1998; 98US-0099763P.		
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PR	PR	10-SEP-1998; 98US-0099808P.		
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PR 18-NOV-1998; 98US-0108851P.  
PR 18-NOV-1998; 98US-0108852P.  
PR 18-NOV-1998; 98US-0108858P.  
PR 18-NOV-1998; 98US-0108904P.  
PR 22-DEC-1998; 98US-0113296P.  
PR 30-DEC-1998; 98US-0114223P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 16-APR-1999; 99US-0129674P.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 15-SEP-1999; 99WO-US021194.  
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PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams FM, Wood WI;  
XX  
DR WPI; 2003-585293/55.  
DR N-PSDB; ACD68321.  
XX  
PT Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,  
PT PRO1787 that modulate glucose or free fatty acid uptake by skeletal  
PT muscle cells, and are useful for treating diabetes, hyper- or hypo-

Query Match 100.0%; Score 1695; DB 6; Length 331;  
Best Local Similarity 100.0%; Pred. No. 1e-165;  
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELAR 60  
Db 1 MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELAR 60  
QY 61 RGGNIILACRDMEXCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIIEEERVDI 120  
Db 61 RGGNIILACRDMEXCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIIEEERVDI 120

QY 121 LINNAGVMRCPHWTTEDGFEMQFGVNHIGHFLLTNLLDLKLKASAPSRRIINSSLAHVAG 180  
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QY 181 HIDFDDLNWQTRKYNTKAAAYCQSKLAIVLFTKELSRRLQSGVTVNALHPGVARTELGRH 240  
Db 181 HIDFDDLNWQTRKYNTKAAAYCQSKLAIVLFTKELSRRLQSGVTVNALHPGVARTELGRH 240  
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RESULT 6

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AC ABO44467;  
XX  
DT 01-OCT-2003 (first entry)  
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XX  
KW Human; secreted protein; transmembrane protein; PRO; vulnery; cardiant;  
KW antidiabetic; anorectic; antiarthritic; angiogenesis; cancer;  
KW adrenal cortical capillary; endothelial cell growth; wound healing;  
KW stimulated T-lymphocyte proliferation; immune response suppression;  
KW neonatal heart hypertrophy; cardiac insufficiency disorder;  
KW vascular endothelial growth factor; inflammation; mononuclear cell;  
KW eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;  
KW chondrocyte redifferentiation; bone disorder; cartilage disorder;  
KW sports injury; arthritis.

OS Homo sapiens.

XX US2003044841-A1.

XX 06-MAR-2003.

PF 06-DEC-2001; 2001US-00006856.

XX 01-SEP-1998; 98US-0098716P.

PR 01-SEP-1998; 98US-0098723P.

PR 01-SEP-1998; 98US-0098749P.

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PR 03-NOV-1998; 98US-0106934P.  
PR 10-NOV-1998; 98US-0107783P.  
PR 17-NOV-1998; 98US-0108775P.  
PR 17-NOV-1998; 98US-0108779P.  
PR 17-NOV-1998; 98US-0108787P.  
PR 17-NOV-1998; 98US-0108788P.  
PR 17-NOV-1998; 98US-0108801P.  
PR 17-NOV-1998; 98US-0108802P.  
PR 17-NOV-1998; 98US-0108806P.  
PR 17-NOV-1998; 98US-0108807P.  
PR 17-NOV-1998; 98US-0108867P.  
PR 17-NOV-1998; 98US-0108925P.  
PR 18-NOV-1998; 98US-0108848P.  
PR 18-NOV-1998; 98US-0108849P.  
PR 18-NOV-1998; 98US-0108850P.  
PR 18-NOV-1998; 98US-0108851P.  
PR 18-NOV-1998; 98US-0108852P.  
PR 18-NOV-1998; 98US-0108858P.  
PR 18-NOV-1998; 98US-0108904P.  
PR 22-DEC-1998; 98US-0113296P.  
PR 30-DEC-1998; 98US-0114223P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 16-APR-1999; 99US-0129674P.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 15-SEP-1999; 99WO-US021194.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;  
XX  
DR WPI; 2003-492259/46.  
DR N-PSDB; ACH04423.  
XX  
PT Novel secreted and transmembrane polypeptides and polynucleotides  
PT encoding them useful for treating various cardiac insufficiency  
PT disorders, bone and/or cartilage disorders such as sports injuries and  
PT arthritis.

Query Match		100.0%;	Score 1695;	DB 7;	Length 331;
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QY	121	LINNAGVMRCPHWTTEDEGFEMQFGVNHGLHFLLTNLLDLKLKASAPSRRIINLSSLAHVAG	180		
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QY	181	HIDFDDLWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQSGVTNALHPGVARTELGRH	240		
Db	181	HIDFDDLWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQSGVTNALHPGVARTELGRH	240		
QY	241	TGIHGSTFSSTTLGPFIWLLVKSPELAAQPSSTYLAVAEELADVSGKYFDGLKQKAPAPEA	300		
Db	241	TGIHGSTFSSTTLGPFIWLLVKSPELAAQPSSTYLAVAEELADVSGKYFDGLKQKAPAPEA	300		
QY	301	EDEEVARRLWAESARLVGLEAPSVREOQLPR	331		
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AC	ABO33491;
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DT	17-SEP-2003 (first entry)
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XX	
KW	Human; secreted and transmembrane protein; PRO; gene therapy; vaccine;
KW	tissue typing; chromosome identification; vaccine.
XX	
OS	Homo sapiens.
XX	
PN	US2003073129-A1.
XX	
PD	17-APR-2003.
XX	
PF	04-SEP-2001; 2001US-00946374.
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PR 17-NOV-1998; 98US-0108802P.  
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PR 18-NOV-1998; 98US-0108848P.  
PR 18-NOV-1998; 98US-0108849P.  
PR 18-NOV-1998; 98US-0108850P.  
PR 18-NOV-1998; 98US-0108851P.  
PR 18-NOV-1998; 98US-0108852P.  
PR 18-NOV-1998; 98US-0108858P.  
PR 18-NOV-1998; 98US-0108904P.  
PR 22-DEC-1998; 98US-00218517.  
PR 22-DEC-1998; 98US-0113296P.  
PR 30-DEC-1998; 98US-0114223P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 12-APR-1999; 99US-00284291.  
PR 16-APR-1999; 99US-0129674P.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 15-SEP-1999; 99WO-US021194.  
PR 18-OCT-1999; 99US-00403297.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 01-JUN-2001; 2001US-00872035.  
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PR 14-JUN-2001; 2001US-00882636.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.

(GETH ) GENENTECH INC.

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy NA, Smith V, Stewart TA, Tumas D, Watanabe CK;

PI Williams PM, Wood WI;  
XX  
DR WPI; 2003-585292/55.  
DR N-PSDB; ACD67967.  
XX  
PT Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the  
PT preparation of a medicament for treating a condition responsive to PRO  
PT polypeptide, and as therapeutic agents e.g. vaccines.  
XX  
PS Claim 12; Fig 66; 561pp; English.  
XX  
CC The invention describes an isolated PRO (secreted and transmembrane)  
CC polypeptide (I), having at least 80% sequence identity to a sequence  
Query Match 100.0%; Score 1695; DB 7; Length 331;  
Best Local Similarity 100.0%; Pred. No. 1e-165;  
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKOTALELAR 60  
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QY 61 RGGNIILACRDMKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVDI 120  
Db 61 RGGNIILACRDMKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVDI 120  
QY 121 LINNAGVMRCPHWTTEDEGFEMQGVNHLGHFLLTNNLLDKLKASAPSRIINLSSLAHVAG 180  
Db 121 LINNAGVMRCPHWTTEDEGFEMQGVNHLGHFLLTNNLLDKLKASAPSRIINLSSLAHVAG 180  
QY 181 HIDFDDLNWQTRKYNNTKAAVCSQKLAIVLFTKELSRRLQSGVTVNALHPGVARTELGRH 240  
Db 181 HIDFDDLNWQTRKYNNTKAAVCSQKLAIVLFTKELSRRLQSGVTVNALHPGVARTELGRH 240  
QY 241 TGIHGSTFSSTTLGPFIWLLVKSPELAAQPSSTYLAVAEELADVSGKYFDGLKQKAPAPEA 300  
Db 241 TGIHGSTFSSTTLGPFIWLLVKSPELAAQPSSTYLAVAEELADVSGKYFDGLKQKAPAPEA 300  
QY 301 EDEEVARRLWAESARLVGLEAPS VREQPLPR 331  
Db 301 EDEEVARRLWAESARLVGLEAPS VREQPLPR 331

RESULT 8

ADC17985  
ID ADC17985 standard; protein; 331 AA.

XX  
AC ADC17985;

XX  
DT 18-DEC-2003 (first entry)

XX  
DE Human PRO polypeptide #33.

XX  
KW Human; PRO; protein electrophoresis; chromosome mapping; gene mapping;  
genetic disorder.

XX  
OS Homo sapiens.

XX  
PN US2003064925-A1.

XX  
PD 03-APR-2003.

XX  
PF 10-DEC-2001; 2001US-00013907.

XX  
PR 01-SEP-1998; 98US-0098716P.

PR 01-SEP-1998; 98US-0098723P.

PR 01-SEP-1998; 98US-0098749P.

PR 01-SEP-1998; 98US-0098750P.

PR 02-SEP-1998; 98US-0098803P.

PR 02-SEP-1998; 98US-0098821P.

PR 02-SEP-1998; 98US-0098843P.

PR 09-SEP-1998; 98US-0099536P.

PR 09-SEP-1998; 98US-0099596P.



PR 09-SEP-1998; 98US-0099598P.  
PR 09-SEP-1998; 98US-0099602P.  
PR 09-SEP-1998; 98US-0099642P.  
PR 10-SEP-1998; 98US-0099741P.  
PR 10-SEP-1998; 98US-0099754P.  
PR 10-SEP-1998; 98US-0099763P.  
PR 10-SEP-1998; 98US-0099792P.  
PR 10-SEP-1998; 98US-0099808P.  
PR 10-SEP-1998; 98US-0099812P.  
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PR 22-DEC-1998; 98US-0113296P.  
PR 30-DEC-1998; 98US-0114223P.  
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PR 26-JUL-1999; 99US-0145698P.  
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PR 15-SEP-1999; 99WO-US021194.  
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PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 01-JUN-2001; 2001WO-US017800.



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PR 28-OCT-1998; 98US-0106029P.  
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PR 03-NOV-1998; 98US-0106856P.  
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PR 05-JAN-1999; 99WO-US000106.  
PR 16-APR-1999; 99US-0129674P.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 15-SEP-1999; 99WO-US021194.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;  
XX  
DR WPI; 2003-874602/81.  
DR N-PSDB; ADD70630.  
XX  
PT Novel isolated PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555,  
PT PRO1787 affect glucose or free fatty acid (FFA) uptake by skeletal muscle  
PT cells and are useful for treating diabetes or hyper- or hypo-insulinemia.  
XX  
PS Claim 12; SEQ ID NO 116; 553pp; English.  
XX  
CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 1695; DB 7; Length 331;  
Best Local Similarity 100.0%; Pred. No. 1e-165;  
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVITGANTGIGKQTALELAR 60  
Db |||||  
1 MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVITGANTGIGKQTALELAR 60  
QY 61 RGGNIILACRDMEKCEAAAKDIRGETLNHHVNNARHLDLASLKSIREFAAKIIIEEERVDI 120  
Db |||||  
61 RGGNIILACRDMEKCEAAAKDIRGETLNHHVNNARHLDLASLKSIREFAAKIIIEEERVDI 120  
QY 121 LINNAGVMRCPHWTTEDEGFEMQFGVNHGLHFLLTNLLDCLKASAPSRRIINLSSLAHVAG 180  
Db |||||  
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Db |||||  
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QY 241 TGIHGSTFSSTTLGPIFWLLVKSPELAACPSTYLAVAEELADVSGKYFDGLKQKAPAPEA 300  
Db |||||  
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Db |||||  
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RESULT 10  
ADD39708  
ID ADD39708 standard; protein; 331 AA.  
XX



ADD39708;  
15-JAN-2004 (first entry)  
Human secreted/transmembrane protein PRO1430.  
Human; secreted protein; transmembrane protein; PRO; tumour;  
immune response; cardiac insufficiency disorder; calcium flux;  
umbilical vein endothelial cell; bone disorder; cartilage disorder;  
arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;  
dermatitis; herpeticiformis; Crohn's disease; thalassaemia.  
Homo sapiens.  
US2003083462-A1.  
01-MAY-2003.  
10-DEC-2001; 2001US-00013913.  
05-JAN-1999; 99WO-US000106.  
01-SEP-1999; 99WO-US020111.  
15-SEP-1999; 99WO-US021194.  
30-NOV-1999; 99WO-US028313.  
02-DEC-1999; 99WO-US028551.  
16-DEC-1999; 99WO-US030095.  
05-JAN-2000; 2000WO-US000219.  
06-JAN-2000; 2000WO-US000376.  
11-FEB-2000; 2000WO-US003565.  
18-FEB-2000; 2000WO-US004342.  
24-FEB-2000; 2000WO-US005004.  
02-MAR-2000; 2000WO-US005841.  
15-MAR-2000; 2000WO-US006884.  
17-MAY-2000; 2000WO-US013705.  
22-MAY-2000; 2000WO-US014042.  
30-MAY-2000; 2000WO-US014941.  
02-JUN-2000; 2000WO-US015264.  
23-AUG-2000; 2000WO-US023522.  
24-AUG-2000; 2000WO-US023328.  
08-NOV-2000; 2000WO-US030952.  
10-NOV-2000; 2000WO-US030873.  
01-DEC-2000; 2000WO-US032678.  
28-FEB-2001; 2001WO-US006520.  
01-MAR-2001; 2001WO-US006666.  
01-JUN-2001; 2001WO-US017800.  
20-JUN-2001; 2001WO-US019692.  
29-JUN-2001; 2001WO-US021066.  
09-JUL-2001; 2001WO-US021735.  
04-SEP-2001; 2001US-00946374.  
(GETH ) GENENTECH INC.  
Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,  
Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,  
Williams PM, Wood WI;  
WPI; 2003-755122/71.  
N-PSDB; ADD39707.  
New secreted and transmembrane PRO polypeptides useful for treating  
cancers, kidney disorders, Crohn's disease, diabetes mellitus, hyper- or  
hypo-insulinemia, sports injuries and arthritis.  
Claim 12; SEQ ID NO 116; 557pp; English.  
The invention relates to an isolated PRO polypeptide (secreted or  
transmembrane protein) having at least 80% amino acid sequence identity  
to an amino acid sequence chosen from 123 fully defined sequences as  
given in the specification (including their extracellular domains either  
or without their associated signal peptides. Also include are the  
nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a

CC	host cell comprising the vector, producing PRO, a chimaeric molecule
CC	comprising PRO fused to a heterologous amino acid sequence, and an anti-
CC	PRO antibody. Pro is useful as molecular weight markers for protein
CC	electrophoresis and also for chromosome identification. PRO is also
CC	useful for tissue typing. PRO and PRO NA are useful as hybridisation
CC	probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is
CC	useful for generating transgenic animals or knock-out animals which are
CC	useful in development and screening useful reagents. PRO NA is also
CC	useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are
CC	useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1419
CC	polypeptides are useful for suppressing immune response. PRO1246
CC	polypeptide is useful for treating cardiac insufficiency disorders.
CC	PRO1246 polypeptide is also useful for treating tumours. PRO1246 and
CC	PRO1561 polypeptide are useful for stimulating calcium flux in human
CC	umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474
CC	polypeptides are useful for treating bone and/or cartilage disorders
CC	(e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO1418
CC	polypeptides are useful for treating diabetes in skeletal muscle cells
CC	and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for
CC	treating Berger disease or other nephropathies associated with Schonlein-
CC	Henoch purpura, coeliac disease, dermatitis, herpetiformis or Crohn's
CC	disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418,
CC	PRO1410 and PRO1575 are useful in treating thalassaemias. The present
CC	sequence represents a PRO protein of the invention.
XX	
SQ	Sequence 331 AA;
	Query Match            100.0%;    Score 1695;   DB 7;   Length 331;
	Best Local Similarity   100.0%;   Pred. No. 1e-165;
	Matches 331;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;
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Dd	1 MSRYLLPLSALGTGAGAAVLLKDYVTGGACPSKATIPGKTIVITGANTGIGKQTALELAR 60
QY	61 RGGNIILACRDMEKCEAAAADIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVDI 120
Dd	61 RGGNIILACRDMEKCEAAAADIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVDI 120
QY	121 LINNAGVMRCPHWTTEDGFEMQFGVNHGLGHFLTNLLDDKLKASAPSRRIINLSSLAHVAG 180
Dd	121 LINNAGVMRCPHWTTEDGFEMQFGVNHGLGHFLTNLLDDKLKASAPSRRIINLSSLAHVAG 180
QY	181 HIDFDDLNMWTRKYNTKAAYCQSKLAIVLFTKELSRRLQGSGVTVNALHPGVARTELGRH 240
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QY	241 TGIHGSTFSSTTLGPFWLLVKSPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAPEA 300
Dd	241 TGIHGSTFSSTTLGPFWLLVKSPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAPEA 300
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Dd	301 EDEEVARRLWAESARLVGLEAPSVREOQLPR 331
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AC	ADD70154;
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DT	15-JAN-2004 (first entry)
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DE	Human secreted/transmembrane protein PRO1430.
XX	
KW	Human; secreted protein; transmembrane protein; PRO; tumour;
KW	immune response; cardiac insufficiency disorder; calcium flux;
KW	umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW	arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW	Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW	dermatitis; herpetiformis; Crohn's disease; thalassaemia.
XX	

OS	Homo sapiens.		
XX	US2003054406-A1.		
PN	20-MAR-2003.		
XX	06-DEC-2001; 2001US-00006818.		
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XX	02-SEP-1998; 98US-0098999P.	PR	16-APR-1999; 99US-0129674P.
XX	02-SEP-1998; 98US-0098999P.	PR	23-JUN-1999; 99US-0141037P.
XX	02-SEP-1998; 98US-0098999P.	PR	20-JUL-1999; 99US-0144758P.
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XX	02-SEP-1998; 98US-0098999P.	PR	01-SEP-1999; 99WO-US020111.
XX	02-SEP-1998; 98US-0098999P.	PR	15-SEP-1999; 99WO-US021194.
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XX	02-SEP-1998; 98US-0098999P.	PR	05-JAN-2000; 2000WO-US000219.
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PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-708344/67.
DR N-PSDB; ADD70153.
XX
PT Novel isolated PRO polypeptide useful for tissue typing, modulating
PT biological activity of cell, as molecular weight markers in protein
PT electrophoresis, for treating arthritis, tumor.
XX
PS Claim 12; SEQ ID NO 116; 549pp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 1695; DB 7; Length 331;
Best Local Similarity 100.0%; Pred. No. 1e-165;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db |||||||
QY 181 HIDFDDLNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQSGSVTVNALHPGVARTELGRH 240
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ADD38275
ID ADD38275 standard; protein; 331 AA.
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AC ADD38275;
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DT 15-JAN-2004 (first entry)
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DE Human secreted/transmembrane protein PRO1430.
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KW Human; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
XX
OS Homo sapiens.
XX
PN US2003096955-A1.
XX
PD 22-MAY-2003.
XX
PF 07-DEC-2001; 2001US-00012755.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
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PR 09-SEP-1998; 98US-0099536P.
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PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
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PR 23-SEP-1998; 98US-0101479P.
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DT	15-JAN-2004 (first entry)		
XX			
DE	Human secreted/transmembrane protein PRO1430.		
XX			
KW	Human; secreted protein; transmembrane protein; PRO; tumour;		
KW	immune response; cardiac insufficiency disorder; calcium flux;		
KW	umbilical vein endothelial cell; bone disorder; cartilage disorder;		
KW	arthritis; wound healing; diabetes; skeletal muscle cells; obesity;		
KW	Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;		
KW	dermatitis; herpeticiformis; Crohn's disease; thalassaemia.		
XX			
OS	Homo sapiens.		
XX			
PN	US2003096954-A1.		
XX			
PD	22-MAY-2003.		
PF	07-DEC-2001; 2001US-00011671.		
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PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
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PR 15-SEP-1999; 99WO-US021194.
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PR 11-FEB-2000; 2000WO-US003565.
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PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US005666.
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PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-786999/74.
DR N-PSDB; ADD39230.
XX
PT Novel isolated PRO polypeptide useful for tissue typing, modulating
PT biological activity of cell, as molecular weight markers in protein
PT electrophoresis, for treating arthritis, tumor.
XX
PS Claim 12; SEQ ID NO 116; 550pp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted or
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Query Match      100.0%; Score 1695; DB 7; Length 331;
Best Local Similarity 100.0%; Pred. No. 1e-165;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB      1 MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELAR 60
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QY      181 HIDFDDLNWQTRKNTKAAQCQSKLAIVLFTKELSRRLQSGVTVNALHPGVARTELGRH 240
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QY      241 TGIHGSTFSSTTLGPIFWLLVKSPELAAQPSSTYLAVAEELADVSGKYFDGLKOKAPAPEA 300
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RESULT 14

ADD38754

ID ADD38754 standard; protein; 331 AA.

XX AC ADD38754;

XX DT 15-JAN-2004 (first entry)

XX DE Human secreted/transmembrane protein PRO1430.

XX KW Human; secreted protein; transmembrane protein; PRO; tumour;  
KW immune response; cardiac insufficiency disorder; calcium flux;  
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;  
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;  
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.

XX OS Homo sapiens.

XX PN US2003092061-A1.

XX PD 15-MAY-2003.

XX PF 06-DEC-2001; 2001US-00007194.

XX PR 01-SEP-1998; 98US-0098716P.  
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PR 16-APR-1999; 99US-0129674P.  
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PR 20-JUL-1999; 99US-0144758P.  
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PR 04-SEP-2001; 2001US-00946374.  
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PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;  
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DR WPI; 2003-765477/72.  
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PT New isolated PRO polypeptide such as PRO1560, PRO444, PRO1018, PRO1773,  
PRO1244, PRO1246, useful for treating cancerous tumors, cardiac

PT insufficiency disorders, wound healing, Crohn's disease, celiac disease.  
XX  
PS Claim 12; SEQ ID NO 116; 555pp; English.  
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CC The invention relates to an isolated PRO polypeptide (secreted or  
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KW immune response; cardiac insufficiency disorder; calcium flux;  
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;  
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;  
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.  
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PN US2003082627-A1.  
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PR 16-APR-1999; 99US-0129674P.  
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PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.

XX (GETH ) GENENTECH INC.  
PA Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;  
XX WPI; 2003-755104/71.  
DR N-PSDB; ADD40184.  
XX New isolated PRO polypeptides such as PRO1560, PRO444, PRO1018, PRO1773,  
PT PRO1244, PRO1246, are useful for treating cancerous tumors and cardiac  
PT insufficiency disorders.  
XX Claim 12; SEQ ID NO 116; 550pp; English.  
PS The invention relates to an isolated PRO polypeptide (secreted or  
XX The invention relates to an isolated PRO polypeptide (secreted or  
CC  
Query Match 100.0%; Score 1695; DB 7; Length 331;  
Best Local Similarity 100.0%; Pred. No. 1e-165;  
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Search completed: June 23, 2004, 11:07:00  
Job time : 64 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 23, 2004, 11:03:04 ; Search time 45 Seconds  
(without alignments)  
2320.812 Million cell updates/sec

Title: US-10-015-393A-116  
Perfect score: 1695  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
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15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archheap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	818	48.3	330	5 Q960C7	Q960c7 drosophila
3	812	47.9	325	5 Q8MZG9	Q8mzg9 drosophila
4	810	47.8	330	5 Q9V4Q3	Q9v4q3 drosophila
5	802.5	47.3	331	5 Q9V4P9	Q9v4p9 drosophila
6	767.5	45.3	300	5 Q9V4Q2	Q9v4q2 drosophila
7	734.5	43.3	300	11 Q9R1R8	Q9r1r8 mus musculu
8	728.5	43.0	293	11 Q9R1R9	Q9r1r9 mus musculu
9	695.5	41.0	296	5 Q8MKN1	Q8mkn1 drosophila
10	668.5	39.4	406	5 Q9W404	Q9w404 drosophila
11	579.5	34.2	309	13 Q7T348	Q7t348 brachydanio
12	569	33.6	303	16 Q7U2X4	Q7u2x4 mycobacteri
13	566	33.4	303	16 O53613	O53613 mycobacteri
14	561	33.1	290	16 Q8EQH7	Q8eqh7 oceanobacil
15	547.5	32.3	321	10 Q9LGI8	Q9lgi8 oryza sativ
16	547	32.3	317	5 Q9VE80	Q9ve80 drosophila

17	534	31.5	311	16	Q7U200	Q7u200 mycobacteri
18	534	31.5	338	16	O53726	O53726 mycobacteri
19	531.5	31.4	304	16	Q9ZBM5	Q9zbm5 mycobacteri
20	530.5	31.3	327	4	Q96BH7	Q96bh7 homo sapien
21	525	31.0	287	5	Q8T0J5	Q8t0j5 drosophila
22	523	30.9	310	16	Q9L2C8	Q9l2c8 streptomyce
23	515	30.4	320	10	P81259	P81259 brassica na
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25	513	30.3	406	5	Q8SZ46	Q8sz46 drosophila
26	511	30.1	331	10	Q8RWJ2	Q8rwj2 arabidopsis
27	504.5	29.8	260	11	Q8BMX8	Q8bm8 mus musculu
28	502	29.6	331	10	Q8LCE7	Q8lce7 arabidopsis
29	497	29.3	321	10	O80924	O80924 arabidopsis
30	492.5	29.1	322	16	Q82D97	Q82d97 streptomyce
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ALIGNMENTS

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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
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RC TISSUE=Placenta;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.  
CC EMBL; BC009881; AAH09881.1; -.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR002198; ADH\_short.  
DR Pfam; PF00106; adh\_short; 1.  
DR PRINTS; PR00080; SDRFAMILY.  
DR PROSITE; PS00061; ADH\_SHORT; 1.  
KW Hypothetical protein; Oxidoreductase.  
SQ SEQUENCE 260 AA; 28794 MW; 12C82526B01A3174 CRC64;

Query Match 79.1%; Score 1340; DB 4; Length 260;  
Best Local Similarity 100.0%; Pred. No. 5.1e-99;  
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	72	MEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVDILINNAGVMRCP	131
Db	1	MEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVDILINNAGVMRCP	60
QY	132	HWTTEGFEQFQVNHGHFLTLNLLDKLKASAPRIINLSSLAHVAGHIDFDDLNWQT	191

Db 61 HWTTEGFMQFGVNHGHLFTLNLLDKLKASAPSRINLSSLAHVAGHIDFDDLNWQT 120

QY 192 RKYNTKAAAYCQSKLAIVLFTKELSRRLQSGVTVNALHPGVARTELGRHTGIHGSTFSST 251

Db 121 RKYNTKAAAYCQSKLAIVLFTKELSRRLQSGVTVNALHPGVARTELGRHTGIHGSTFSST 180

QY 252 TLGPFIWLLVKSPELAAQSPSTYLAVAEELADVSGKYFDGLKQKAPAPAEADEEVARRLWA 311

Db 181 TLGPFIWLLVKSPELAAQSPSTYLAVAEELADVSGKYFDGLKQKAPAPAEADEEVARRLWA 240

QY 312 ESARLVGLEAPSVREQPLPR 331

Db 241 ESARLVGLEAPSVREQPLPR 260

RESULT 2

Q960C7

ID Q960C7 PRELIMINARY; PRT; 330 AA.

AC Q960C7;

DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE SD07613p.

GN CG2064 OR BCDNA:SD07613.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,

RA Gonzales M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,

RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanenvong S., Wan K.,

RA Yu C., Lewis S.E., Rubin G.M., Celniker S.,

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.

DR EMBL; AY052124; AAK93548.1; -.

DR FlyBase; FBgn0033205; CG2064.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR002198; ADH\_short.

DR Pfam; PF00106; adh\_short; 1.

DR PRINTS; PR00080; SDRFAMILY.

KW Oxidoreductase.

SQ SEQUENCE 330 AA; 36591 MW; 1D941F466B2554F5 CRC64;

Query Match 48.3%; Score 818; DB 5; Length 330;

Best Local Similarity 53.9%; Pred. No. 4e-57;

Matches 171; Conservative 44; Mismatches 100; Indels 2; Gaps 2;

QY 5 LLPLSALGTVAGAAV-LLKDYVTGGACPSKATIPGKTVIVTGANTGIGKGTALARRGG 63

Db 9 LSPLIMFPATIGVGIIYFLKEYMQGGKFTKQDETGKVFIVTGANTGIGKGTALARRGG 68

QY 64 NIIACRDMKECAAAKDITGETLNHHVNHARHLDLASLKSIREFAAKIIEBEERVVDILIN 123

Db 69 TVYLACRDMNRCEKARKDIIKETNNQNIIFSRELDLSLDSIRKFVDGFKKQPKLHVLIN 128

QY 124 NAGVMRCPHWTTEDGFEMQFVNHGHLGHLFTLNLLDKLKASAPSRINLSSLAHVAGHID 183

Db 129 NAGVMRCPKTLTKDGYELQGLGVNHIGHFLLTNLLDLVLKNSAPSRIVVSSLAHARGGIN 188

QY 184 FDLNWQTRKYNTKAAAYCQSKLAIVLFTKELSRRLQSGVTVNALHPGVARTELGRHTGI 243

Db 189 VADLN-SEKSYDEGLAYSQSKLANVLFTRELAKRLEGSGVTVNALHPGVVDTLARNWAF 247

QY 244 HGSTFSSTTLGPIFWLLVKSPELAAQSPSTYLAVAEELADVSGKYFDGLKQKAPAPAEADE 303

Db 248 FQTNLVKFFLKPMIWPLLLKTPKSGAQTISIYAALDPELKNISGLYFSDCKPKVPAPGALDD 307

QY 304 EVARRLWAESARLVGLE 320

Db 308 KVAKFLWAESEKWTGLD 324

RESULT 3

Q8MZG9

ID Q8MZG9 PRELIMINARY; PRT; 325 AA.

AC Q8MZG9; Q9V4Q1;

DT 01-OCT-2002 (TREMBlrel. 22, Created)

DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE LF06328p (CG2070-PA).

GN CG2070.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkely;

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,

RA George R., Gonzales M., Guarin H., Kronmiller B., Li P., Liao G.,

RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,

RA Patel S., Phouanenvong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,

RA Celniker S.,

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=20196006; PubMed=107311132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,

RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Balleg R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Spivars R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,

RA Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

RN [3]

RP SEQUENCE FROM N.A.

RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,





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RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL EMBL; AE003840; AAF59212.3; -.
DR EMBL; AE003840; AAF59212.3; -.
DR FlyBase; FBgn033205; CG2064.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
SQ SEQUENCE 330 AA; 36581 MW; 1D941F46681567F5 CRC64;

Query Match 47.8%; Score 810; DB 5; Length 330;
Best Local Similarity 53.6%; Pred. No. 1.7e-56;
Matches 170; Conservative 44; Mismatches 101; Indels 2; Gaps 2;

QY 5 LLPLSALGTVAGAAV-LLKDYVTGACPSKATIPGKTVIVTGANTGIGKQTALRLARRGG 63
Db 9 LSPLMWPATIGVGIIYFLKEYMQGKFTKDTDTGKVFIVTGANTGIGKETALEIARRGG 68
QY 64 NIILACRDMEKCEAAKDIRGEIINHVNARHLDLASLKSIREFAAKIIEEERVDILIN 123
Db 69 TVYLACRDNRCEKARKDIIKETNNQIFSRDLSSLSIRKFDVGFKKEQPKLHVLIN 128
QY 124 NAGVMRCPHWTTEDGFEMQFGVNHGHFLLTNLLDLKLKASAPSRINLSSLAHVAGHID 183
Db 129 NAGVMRCPKTLTKDGYELQLGVNHGHFLLTNLLDLVKNAPSRIVVSSLAHARGSIN 188
QY 184 FDDLWQTRKYNTKAAAYCQSKLAIVLFTKELSRRLQSGVTNNALHPGVARTELGRHTGI 243
Db 189 VADLN-SEKSYDEGLAYSQSKLANVLFTRELAKRLEGSGVTNNALHPGVVDTELARNWAF 247
QY 244 HGSTFSSTLIGPIFWLLVKSPELAAQSPSTYLAVAEELADVSGKYFDGLKQKAPAEAEDE 303
Db 248 FQTNLVKFLKPMIWPPLLLKTPKSGAQTISIYALDPELNISGLYFSDCKPKPVASGALDD 307
QY 304 EVARRLWAEARLVGLE 320
Db 308 KVAKFLWAESEKWTGLD 324

RESULT 5
Q9V4P9 PRELIMINARY; PRT; 331 AA.
AC Q9V4P9; Q9V4P8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG30491 protein (AT09608p).
GN CG30495 OR CG17986.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostali D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,
Mout S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
[2]
SEQUENCE FROM N.A.
Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Ferrera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
"Sequencing of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
"Annotation of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE FROM N.A.
Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[5]
SEQUENCE FROM N.A.
FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
[6]
SEQUENCE FROM N.A.
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.;
Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AE003840; AAF59216.3; -.
DR EMBL; AY122067; AAM52579.1; -.

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DR HSSP; P50162; 1AE1.  
DR FlyBase; FBgn0050491; CG30491.  
DR FlyBase; FBgn0050495; CG30495.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR002198; ADH\_short.  
DR Pfam; PF00106; adh\_short; 1.  
DR PRINTS; PR00080; SDRFAMILY.  
SQ SEQUENCE 331 AA; 37137 MW; 59B1F6D5453BDC4B CRC64;  
  
Query Match 47.3%; Score 802.5; DB 5; Length 331;  
Best Local Similarity 52.2%; Pred. No. 6.9e-56;  
Matches 164; Conservative 44; Mismatches 105; Indels 1; Gaps 1;  
  
QY 2 SRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARR 61  
Db 9 SRTAEWLSFTGTTTGLAFFVKDLMQGGQFTKETNETGKVFIVTGANTGIGKTVREIAKR 68  
  
QY 62 GGNIIILACRDMKECAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEERVDIL 121  
Db 69 GGTVMACRLNKKCEEARZEEIVLETKNKYVYCRQCCLASQESIRHFVAAFKEQEHVL 128  
  
QY 122 INNAGVMRCPHWTTEDEGFEMQFGVNHGLHLLTNLLDLKLKASAPSRINLSSLAHVAGH 181  
Db 129 INNAGVMRCPRLSTSDGIELQLGVNHMGHLLTNLLDLKLKSSPSRVNVSSLAHTRGE 188  
  
QY 182 IDFDLNLWQTRKYNKTAAYCQSKLAIVLFTKELSRRLQSGVTVNALHPGVARTELGRHT 241  
Db 189 INTGDLN-SDKSYDEGKAYSQSKLANVLTRELAKRLEGNVTANALHPGVVDTEIRHM 247  
  
QY 242 GIHGSFSSSTTLGPIFWLLVKSPELAAQPSSTYLAVAEELADVSGKYFDGLKQKAPAEAE 301  
Db 248 GFFNNFFAGLVKPLFWFPFKTPRNGAQTSLYVALDPELEKVTGQYFSDCKLKEMAPAAT 307  
  
QY 302 DEEVARRLWAEASAR 315  
Db 308 DTQTAKWLWAVSEK 321  
  
RESULT 6  
Q9V4Q2  
ID Q9V4Q2 PRELIMINARY; PRT; 300 AA.  
AC Q9V4Q2;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE CG2065 protein (RH23455p).  
GN CG2065.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkeley;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Fosier C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195 (2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkeley;  
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,  
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,  
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
RA Celniker S.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
CC (SDR) FAMILY.  
DR EMBL; AE003840; AAF59213.1; -.  
DR EMBL; AY071710; AAL49332.1; -.  
DR FlyBase; FBgn0033204; CG2065.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR002198; ADH\_short.  
DR Pfam; PF00106; adh\_short; 1.  
DR PRINTS; PR00080; SDRFAMILY.  
KW Oxidoreductase.  
SQ SEQUENCE 300 AA; 33378 MW; 4FE7A159BD57FACA CRC64;  
  
Query Match 45.3%; Score 767.5; DB 5; Length 300;  
Best Local Similarity 51.3%; Pred. No. 3.8e-53;  
Matches 153; Conservative 50; Mismatches 94; Indels 1; Gaps 1;  
  
QY 27 GGACPSKATIPGKTVIVTGANTGIGKQTALELARRGNNIILACRDMKECAAAKDIRGET 86  
Db 3 GGQFTKQTDETGKVFIVTGANTGIGKETVLEIAKRGGTVYMACRDMNRCEKARQDIIRET 62  
  
QY 87 LNHVNARHLDLASLKSIREFAAKIIEEERVDILINNAGVMRCPHWTTEDEGFEMQFGVN 146  
Db 63 NNQNIIFSRELDLSSLESIRKFAAGFKQDKLHVLIINNAGVMHCPRTLTKDGFEMQLGVN 122  
  
QY 147 HLGHFLLTNLLDLKLKASAPSRINLSSLAHVAGHIDFDLNLWQTRKYNKTAAYCQSKLA 206  
Db 123 HMGHFLLTNLLDLVLKKTAPSRIVNVSSILVHTQGFIKTADLN-SEKSYSRIGAYSQSKLA 181  
  
QY 207 IVLFTKELSRRLQSGVTVNALHPGVARTELGRHTGIHGSTFSSTLIGPIFWLLVKSPEL 266  
Db 182 NVLFTRELAKRLEGTGVTNSLHPGAVDTELSRNWKFHKHPFAQLLLKPLLVLFKTPRN 241  
  
QY 267 AAQPSSTYLAVAEELADVSGKYFDGLKQKAPAEAEDEEVARRLWAEASARLVGLEAPSV 324  
Db 242 GAQTTLYAALDPAKLDVSGLYFSDCQPKVSAQAQDDKTGKFLWAESEKWTGVNSTKV 299  
  
RESULT 7  
Q9R1R8  
ID Q9R1R8 PRELIMINARY; PRT; 300 AA.

AC Q9R1R8;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE UBE-1b.  
GN RDH11 OR ARSDR1 OR UBE-1B.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CD-1; TISSUE=Testis;  
RA Goto M., Eddy E.M.;  
RT "Ubiquitously expressing gene.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
CC (SDR) FAMILY.  
CC EMBL; AB030504; BAA82657.1; -.  
DR MGD; MGI:102581; Rdh11.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR002198; ADH\_short.  
DR Pfam; PF00106; adh\_short; 1.  
DR PRINTS; PR00080; SDRFAMILY.  
KW Oxidoreductase.  
SQ SEQUENCE 300 AA; 33240 MW; 7322230DB9057262 CRC64;  
  
Query Match 43.3%; Score 734.5; DB 11; Length 300;  
Best Local Similarity 50.2%; Pred. No. 1.6e-50;  
Matches 151; Conservative 51; Mismatches 92; Indels 7; Gaps 2;  
  
QY 19 VLLKDYVTGGACPSKATIPGKTVITGANTGIGKQTALRLARRGGNIILACRDMKCEAA 78  
Db 3 LVLRKMLSSGVCTSNVQLPGKVAITGANTGIGKETAQDLAQRGARVYLACRDVDKGELA 62  
  
QY 79 AKDIRGETLNHHVNARHLDLASLKSIREFAAKIIIEEERVDILINNAGVMRCPHWTTEG 138  
Db 63 AREIQAVTGNQVFRVKLDLADTKSIRAFKDFLAEEKHLHLINNAGVMRCPYSKTADG 122  
  
QY 139 FEMQFGVNHGLHFLTLNLLDKLKASAPRIINLSSLAHVAGHIDFDDLNWQTRKYNTKA 198  
Db 123 FEMHIGVNHGLHFLTLHLLLEKLESAPSRIIVNLSLGHILGRHFNHNLQGE-KFYSAGL 181  
  
QY 199 AYCQSKLAIVLFTKELSRRLQSGVTVNALHPGVARTELGRHTGIHGSTFSSITLGPFW 258  
Db 182 AYCHSKLANLFTKELAKRLKSGVTVSVHPGTVHSELTRYSSI-----MRWLWQLFF 235  
  
QY 259 LLVKSPELAQSPSTYLAVAEELADVSGKYFDGLKQKAPAPAEDEEVARRLWAEARLVG 318  
Db 236 VFIKTPQEGAGTSLYCALTEGLESLSGSHFSDCQLAWVSQGRNEIARRLDVSCDLLG 295  
  
QY 319 L 319  
Db 296 L 296  
  
RESULT 8  
Q9R1R9 PRELIMINARY; PRT; 293 AA.  
AC Q9R1R9;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE UBE-1a.  
GN RDH11 OR ARSDR1 OR UBE-1A.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Goto M., Eddy E.M.;

RT "Isolation of ubiquitously expressing mouse genes.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
CC (SDR) FAMILY.  
CC EMBL; AB030503; BAA82656.1; -.  
DR MGD; MGI:102581; Rdh11.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR002198; ADH\_short.  
DR Pfam; PF00106; adh\_short; 1.  
DR PRINTS; PR00080; SDRFAMILY.  
KW Oxidoreductase.  
SQ SEQUENCE 293 AA; 32442 MW; 1C4FFA9770F0E9D0 CRC64;  
  
Query Match 43.0%; Score 728.5; DB 11; Length 293;  
Best Local Similarity 50.8%; Pred. No. 4.8e-50;  
Matches 150; Conservative 48; Mismatches 90; Indels 7; Gaps 2;  
  
QY 25 VTGGACPSKATIPGKTVITGANTGIGKQTALRLARRGGNIILACRDMKCEAAKDIRG 84  
Db 2 LSSGVCTSNVQLPGKVAITGANTGIGKETAQDLAQRGARVYLACRDVDKGELAAREIQ 61  
  
QY 85 ETLNHHVNARHLDLASLKSIREFAAKIIIEEERVDILINNAGVMRCPHWTTEGPFEMQFG 144  
Db 62 VTGNSQVFRVKLDLADTKSIRAFKDFLAEEKHLHLINNAGVMRCPYSKTADGPFEMHIG 121  
  
QY 145 VNHGLHFLTLNLLDKLKASAPRIINLSSLAHVAGHIDFDDLNWQTRKYNTKAAYCQSK 204  
Db 122 VNHGLHFLTLHLLLEKLESAPSRIIVNLSLGHILGRHFNHNLQGE-KFYSAGLAYCHSK 180  
  
QY 205 LAIVLFTKELSRRLQSGVTVNALHPGVARTELGRHTGIHGSTFSSITLGPFWLLVKSP 264  
Db 181 LANILFTKELAKRLKSGVTVSVHPGTVHSELTRYSSI-----MRWLWQLFFVFIKTP 234  
  
QY 265 ELAAQSPSTYLAVAEELADVSGKYFDGLKQKAPAPAEDEEVARRLWAEARLVGL 319  
Db 235 QEGAQTSLYCALTEGLESLSGSHFSDCQLAWVSQGRNEIARRLDVSCDLLGL 289  
  
RESULT 9  
Q8MKN1 PRELIMINARY; PRT; 296 AA.  
ID Q8MKN1;  
AC Q8MKN1;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE CG30495-PA.  
GN CG30495 OR CG17986.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkely;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,



RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulo G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RA "The genome sequence of Drosophila melanogaster";  
RT Science 287:2185-2195(2000).  
RL [2]  
RN

RP SEQUENCE FROM N.A.  
RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,  
RA Evans C.A., Gocayne J.D., Ananatides P.G., Brandon R.C., Rogers Y.,  
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,  
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,  
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,  
RA Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,  
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
RA "Sequencing of Drosophila melanogaster genome";  
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RL [3]  
RN

RP SEQUENCE FROM N.A.  
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,  
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,  
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
RA Kronmiller B., Marshall B., Milburn G., Richter J., Russo S.,  
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,  
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
RA "Annotation of Drosophila melanogaster genome";  
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RL [4]  
RN

RP SEQUENCE FROM N.A.  
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RL [5]  
RN

RP SEQUENCE FROM N.A.

RA FlyBase;

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
(SDR) FAMILY.

CC EMBL; AE003840; AAM71103.1; -.

DR FlyBase; FBgn0050495; CG30495.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR002198; ADH short.

DR Pfam; PF00106; adh short; 1.

DR PRINTS; PR00080; SDRFAMILY.

KW Oxidoreductase.

SQ SEQUENCE 296 AA; 33041 MW; 3672588F9E4E8EBF CRC64;

Query Match

Best Local Similarity 41.0%; Score 695.5; DB 5; Length 296;

Matches 142; Conservative 54; Mismatches 92; Indels 1; Gaps 1;

QY 27 GGACPSKATIPGKTVITGANTGIGKOTALELARRGNIILACRDMEKCEAAKDIRGET 86  
Db 3 GGFRRKQTDGKVAIVTGGTGLGKETVMELARRGATVYMACRNKEKVERARREIVKET 62  
QY 87 LNHVNVNARHLDSLKSIREFAAKIIEEERVDILINNAGVMRCPHWTTEDGEMQFGVN 146  
Db 63 GNSNVFSRECDLSSLDLSIRKFAENFKKEQORVLHILINNAGVFWPEHRLTKEGFEMHLGVN 122  
QY 147 HLGHFLLTNLLDKLKASAPSRRIINLSSLAHVAGHIDFDLNNQWTRKYNTKAAYCQSKLA 206  
Db 123 HIGHFLTNLLGLVLSAPSRVWVASRAHERGQIKVDDIN-SSDFYDEGVAYCQSKLA 181  
QY 207 IVLFTKELSRRLQSGVTVNALHPGVARTELGRHTGIHGSTFSSTLGPFWLLVKSP 266  
Db 182 NLFTRRELAKRLEGTGTVNALNPGIADTEIARNMIFFTQKFAQTILRPLLWAVMKTPKN 241  
QY 267 AAQPSLYLAVAEELADVSGKYFDGLKQKAPAPAEDEEVARRLWAESAR 315  
Db 242 GAQTTLYAALDPDLERSVSGQFSDCALAPVAPALDDQMAQLWAQSEK 290

RESULT 10

Q9W404

ID Q9W404 PRELIMINARY; PRT; 406 AA.

AC Q9W404;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE CG3842 protein.

GN CG3842.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkely;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Balaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhattacharya D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Ke Z., Kennison J.A., Ketchum K.A.,

RA Jalali M., Kalush F., Karpen G.H., Kravitz S., Kulp D., Lai Z.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulo G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,









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OM nucleic - nucleic search, using sw model

Run on: June 23, 2004, 11:04:52 ; Search time 139 Seconds  
(without alignments)  
7218.354 Million cell updates/sec

Title: US-10-015-393A-115  
Perfect score: 1808  
Sequence: 1 gagctaccaggcggtgtgt.....actctcaacttgctcattt 1808

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCUTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	532	29.4	1352	4	US-09-833-381-931
2	297.8	16.5	2494	4	US-09-724-864-6
3	247.8	13.7	2507	4	US-09-439-313-332
4	247.8	13.7	2507	4	US-09-352-616A-332
5	247.8	13.7	2507	4	US-09-232-149A-332
6	247.8	13.7	2507	4	US-09-636-215-332
7	247.8	13.7	2507	4	US-09-685-166A-332
8	247.8	13.7	2507	4	US-09-688-489-332
9	233.2	12.9	1086	1	US-08-464-400-1
10	233.2	12.9	1086	3	US-08-875-273A-1
11	233.2	12.9	1086	4	US-09-123-386-1
12	233.2	12.9	1086	5	PCT-US95-01827A-1
13	219.6	12.1	234	4	US-09-833-381-933
14	168.2	9.3	4403765	3	US-09-103-840A-2
15	166.6	9.2	4411529	3	US-09-103-840A-1
C 16	139.8	7.7	337	4	US-09-439-313-385
C 17	139.8	7.7	337	4	US-09-352-616A-385
C 18	139.8	7.7	337	4	US-09-636-215-385
C 19	139.8	7.7	337	4	US-09-685-166A-385
C 20	139.6	7.7	1376	4	US-09-489-847-66
C 21	138.8	7.7	4403765	3	US-09-103-840A-2
C 22	138.8	7.7	4411529	3	US-09-103-840A-1
23	131.2	7.3	1143	4	US-09-252-991A-16283
24	131.2	7.3	1383	4	US-09-252-991A-16511
C 25	131.2	7.3	2400	4	US-09-252-991A-15991
26	127.2	7.0	1375	4	US-09-489-847-120
27	122.4	6.8	2310	4	US-09-620-312D-206

C	28	106	5.9	222	4	US-09-833-381-932	Sequence 932, App
	29	93.8	5.2	1378	2	US-08-580-545B-1	Sequence 1, Appli
	30	93.8	5.2	1378	3	US-09-262-653A-1	Sequence 1, Appli
	31	88	4.9	1197	2	US-08-530-165-6	Sequence 6, Appli
	32	80.2	4.4	864	2	US-08-901-306-1	Sequence 1, Appli
	33	80.2	4.4	864	3	US-09-180-271-1	Sequence 1, Appli
	34	80.2	4.4	1569	2	US-08-901-306-3	Sequence 3, Appli
	35	80.2	4.4	1569	3	US-09-180-271-3	Sequence 3, Appli
	36	78.8	4.4	825	4	US-09-328-352-4087	Sequence 4087, Ap
	37	71	3.9	771	4	US-09-252-991A-13903	Sequence 13903, A
	38	71	3.9	1419	4	US-09-252-991A-13796	Sequence 13796, A
	39	71	3.9	1995	4	US-09-252-991A-13546	Sequence 13546, A
	40	68.8	3.8	268	4	US-09-313-294A-2451	Sequence 2451, Ap
	41	54.4	3.0	3196	2	US-09-096-982-4	Sequence 4, Appli
	42	54.4	3.0	3196	2	US-08-653-650A-4	Sequence 4, Appli
	43	53	2.9	1138	3	US-08-581-148C-3	Sequence 3, Appli
	44	51	2.8	948	4	US-09-252-991A-9617	Sequence 9617, Ap
	45	51	2.8	3162	4	US-09-252-991A-9569	Sequence 9569, Ap

ALIGNMENTS

RESULT 1  
US-09-833-381-931/c  
; Sequence 931, Application US/09833381  
; Patent No. 6672186  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs  
; FILE REFERENCE: 5800-119  
; CURRENT APPLICATION NUMBER: US/09/833,381  
; CURRENT FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: 09/516,448  
; PRIOR FILING DATE: 2000-02-29  
; NUMBER OF SEQ ID NOS: 2050  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 931  
; LENGTH: 1352  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(1352)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-833-381-931

Query Match	29.4%;	Score 532;	DB 4;	Length 1352;
Best Local Similarity	81.7%;	Pred. No. 3.9e-116;		
Matches	638;	Conservative	0;	Mismatches 113; Indels 30; Gaps 1;
QY	420	AGAGGAGGAGCGGAGTGGACATTCTAATCAACAACCGGGGTGTGATGGGTGCCCCACTG	479	
Db	1300	AGAGGAGGAGCGGAGTGGACATTCTAATCAACAACCGGGGTGTGATGGGTGCCCCACTG	1241	
QY	480	GACCAACCGAGGACGGCTTCGAGATGCAGTTTGGCGTTAACCCACCTGGGTCACTTTCTCTT	539	
Db	1240	GACCAACCGAGGACGGNTTCGAGATGCAGNTTGGCGTTAACCCACCTGGGTCACTTTCTCTT	1181	
QY	540	GACAAACTTGCTGCTGGACAAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTC	599	
Db	1180	GACAAACTTGCTGCTGGACAAGCTGAAAGCCTTCGCGGATCATCAACCTCTC	1121	
QY	600	GTCCCTGGCCCATGTTGCTGGGCACATAGACTTTGACGACTTGAACCTGGCAGACGAGGAA	659	
Db	1120	GTCCCTGGCCCATGTTGCTGGGCACATAGACTTTGACGACTTGAACCTGGCAGACGAGGAA	1061	
QY	660	GTATAACACCAAGCCGCTACTGCCAGAGCAAGCTGCCCATCGTCTCTTCAACCAAGGA	719	
Db	1060	GTATAACACCAAGCCGCTACTGCCAGAGCAAGCTGCCCATCGTCTCTTCAACCAAGGA	1001	
QY	720	GCTGAGCCCGGGCTGCAAGGCTCTGGTGTGACTGTCAACGCCCTGCACCCGGCGTGGC	779	

Db 1000 GGTGAGCGGGGGCTTCACGGTTCTGGTGTGACTGTCAACGCCCTTCTCTCAAGCGTCGG 941  
QY 780 CAGGACAGAGCTGGGC-----AGACACACGGGCAT 809  
Db 940 GGAGGACGGCCAGGGCTGTCTGGCGGATGAGAAACCGTGTCTCAGAGGAAGGACGTG 881  
QY 810 CCATGGCTCCACCTTCTCCAGCACACACTCGGGCCCATCTTCTGGCTGTCTGGTCAAGAG 869  
Db 880 GTGCTGACGCTGGAGTCAGGCTGTACTCAGGGGCCCATCTTCTGGCTGTCTGGTCAAGAG 821  
QY 870 CCCCAGCTGGCCGCCAGCCAGCCAGACATACCTGGCCGTGGCGGAGGAACCTGGCGGATGT 929  
Db 820 CCCCAGCTGGCCGCCAGCCAGCCAGACATACCTGGCCGTGGCGGAGGAACCTGGCGGATGT 761  
QY 930 TTCCGGAAAGTACTTCGATGGACTCAAAACAGAGGCCCGCCCGCTGGTGGGCTTAGAGGCTCCCTC 1049  
Db 760 TTCCGGAAAGTACTTCGATGGACTCAAAACAGAGGCCCGCCCGCTGGTGGGCTTAGAGGCTAGGA 701  
QY 990 GGAGGTGGCCCGGAGGCTTTGGGCTGAAAGTGCCTGGTGGGCTTAGAGGCTCCCTC 1049  
Db 700 GGAGGTGGCCCGGAGGCTTTGGGCTGAAAGTGCCTGGTGGGCTTAGAGGCTCCCTC 641  
QY 1050 TGTGAGGAGCAGCCCTCCAGACATAACCTCTGGAGCAGATTGAAAGCCAGGATGGCG 1109  
Db 640 CTTGGGGGGGTACCCCCCCCCCTGTAAACCTCGGGGCCATTTAAAGCCCGTAGTGG 581  
QY 1110 CCTCCAGACCGAGGACAGCTGTCCGCCATGCCCCGAGCTTCTGGCACTACCTGAGCCGG 1169  
Db 580 CCCTCGAGCGGGGCCACCGATCCATCCATTCGCTCATTTGTGCCCCACTAACCTGGGTGG 521  
QY 1170 G 1170  
Db 520 G 520

RESULT 2  
US-09-724-864-6  
; Sequence 6, Application US/09724864  
; Patent No. 6380362  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Murison, James G.  
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed  
; TITLE OF INVENTION: by the polynucleotides and methods for their use.  
; FILE REFERENCE: 11000.1050U1  
; CURRENT APPLICATION NUMBER: US/09/724,864  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 2494  
; TYPE: DNA  
; ORGANISM: Rat  
US-09-724-864-6  
Query Match 16.5%; Score 297.8; DB 4; Length 2494;  
Best Local Similarity 80.1%; Pred. No. 6.8e-61;  
Matches 366; Conservative 0; Mismatches 82; Indels 9; Gaps 1;  
QY 638 ACTTGAACTGGCAGACGAGGAAGTATAACACCAAGCCGCTACTGCCAGAGCAAGCTCG 697  
Db 1 ACTTGAACTGGCAGATAAAAGATATGACACCAAGGCAGCTTACTGCCAGAGCAAGTTGG 60  
QY 698 CCATCGTCTCTTACCAAGGAGCTGAGCCGGCGGCTGCAAGGCTCTGGTGTGACTGTCA 757  
Db 61 CTGTTGTCTCTTACCAAGGAGCTGAGTCGCCGGCTGCAAGGCAGCTGGTGTGACTGTCA 120  
QY 758 AGCCCTGCACCCCGGCTGGCCAGGACAGAGCTGGGCGAGACACACGGGCATCCATGGCT 817  
Db 121 ATGCGCTGCACCCCTGGCTGGCCAGGACGGAGCTGGGGCGACATACAGGCATGCACAACT 180

QY 818 CCACCTTCTCCAGCACACACTCGGGCCCCATCTTCTGGCTGTCTGGTCAAGAGCCCGCAGC 877  
Db 181 CTGCGTCTCTGGCTTCAATGCTTGGGCCCTTCTTCTGGCTGTCTTCAAGAGTCCCGCAGC 240  
QY 878 TGGCGGCCAGCCAGCCAGCACATACCTGGCCGTGGCGGAGGAACCTGGCGGATGTTTCCGGA 937  
Db 241 TGGCGGCCAGCCAGCCAGCACATACCTGGCTGTGGCAGAGGAACCTGGAGAGTGTCTCTGGA 300  
QY 938 AGTACTTCGATGGACTCAAAACAGAAAGGCCCGCCCGCTGGTGGGCTTAG-----AGGCTCCCT 997  
Db 301 AGTACTTCGATGGACTCAGAGAAAGGCTCCATCTCTGAGGCTGAAGATGAGGAAGTAG 360  
QY 998 CCCGAGGCTTTGGGCTGAAAGTGCCTGGCTGGTGGGCTTAG-----AGGCTCCCT 1048  
Db 361 CCCGAGGCTTTGGACTGAAAGTGCCTATTTGGTGGGCTTGACATGGCTCATGGGTCCT 420  
QY 1049 CTGTAGGAGCAGCCCTCCAGATAACCTCTGGA 1085  
Db 421 CTGGAGAGGACATTCCATCTCCAGATAACCTTCAGA 457

RESULT 3  
US-09-439-313-332  
; Sequence 332, Application US/09439313  
; Patent No. 6329505  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan Louise  
; APPLICANT: Jiang Yuqui  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Kalos, Michael  
; APPLICANT: Fanger, Gary  
; APPLICANT: Retter, Mark  
; APPLICANT: Solk, John  
; APPLICANT: Day, Craig  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C9  
; CURRENT APPLICATION NUMBER: US/09/439,313  
; CURRENT FILING DATE: 1999-11-12  
; NUMBER OF SEQ ID NOS: 575  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 332  
; LENGTH: 2507  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-439-313-332

Query Match 13.7%; Score 247.8; DB 4; Length 2507;  
Best Local Similarity 55.3%; Pred. No. 4.1e-49;  
Matches 536; Conservative 0; Mismatches 412; Indels 21; Gaps 2;  
QY 130 GCCGCGTGTCTCAAGGACTATGTACCCGGTGGGGCTTGGCCAGCAAGGCCCATC 189  
Db 81 GCTGCGCCCAATCAGGAAATGCTGTCCAGTGGGTGTATCATCAACTGTTTCAGCTT 140  
QY 190 CCTGGGAAGACGGTCATCGTGACGGCGCCCAACACAGGCATCGGGAAGCAGACCGCTTG 249  
Db 141 CCTGGGAAGTAGTGTGTGTCAAGAGCTAATACAGGTATCGGGAAGGAGACAGCCAAA 200  
QY 250 GAACTGGCCAGGAGAGGAGCAACATCATCTTGGCTTGGCCAGACATGGAGAAGTGTGAG 309  
Db 201 GAGCTGGCTCAGAGAGGAGCTCGAGTATATTAGCTTGGCCGGATGTGGAAGGGGGA 260  
QY 310 GCGGCAGCAAGGACATCCGCGGGGAGACCCCTCAATCAATCATGTCAACGCCCGGCACCTG 369  
Db 261 TTGGTGGCCAAAGAGATCCAGACCAGCAGGGAACCCAGCAGGTGTGTTGTCGGAAACTG 320  
QY 370 GACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAGATATGAGAGGAGGAG 429  
Db 321 GACCTGTCTGATACTAAGTCTATTCCAGCTTTTGTAGGGCTTCTTAGCTGAGGAAG 380





RESULT 5  
US-09-232-149A-332  
; Sequence 332, Application US/09232149A  
; Patent No. 6465611  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer Lynn  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE  
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.427C6  
; CURRENT APPLICATION NUMBER: US/09/232,149A  
; CURRENT FILING DATE: 1999-01-15  
; NUMBER OF SEQ ID NOS: 338  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 332  
; LENGTH: 2507  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-232-149A-332

Query Match 13.7%; Score 247.8; DB 4; Length 2507;  
Best Local Similarity 55.3%; Pred. No. 4.1e-49;  
Matches 536; Conservative 0; Mismatches 412; Indels 21; Gaps 2;

QY 130 GCCGCCGTGCTCAAGGACTATGTCACCGGTGGGCTTGGCCCGCAGCAGCCACCATC 189  
|||  
Db 81 GCTGCCCCCAATCAGGAAATGCTGCCAGTGGGTGTATCATCACTGTTGAGCTT 140  
|||  
QY 190 CCTGGGAAGACGGTCACTGTCAGCGGCGCCCAACACAGGCATCGGGAAGCAGCCCTTG 249  
|||  
Db 141 CCTGGGAAGTAGTTGTGTCACAGGAGCTAATACAGGTATCGGGAAGGAGACAGCCAAA 200  
|||  
QY 250 GAATGCGCAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 309  
|||  
Db 201 GAGTGGCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 260  
|||  
QY 310 GCGGCAAGAAAGGACATCCGCGGGGAGACCTCAATCACTGTCACCGCCCGCACCTG 369  
|||  
Db 261 TTGGTGGCAAAAGAGATCCAGACCAAGGAAACAGGAGGTGTTGGTGGCGGAACTG 320  
|||  
QY 370 GACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAGATCATTTGAAGAGGAGGAG 429  
|||  
Db 321 GACCTGCTGATCTAAGTCTATTCCAGCTTTTGCTAAGGCTTCTTAGCTGAGGAAAG 380  
|||  
QY 430 CGAGTGGACATTTCTAATCAACAAACGCGGTGTGATCGGTGCCCCCACTGGACCCAGG 489  
|||  
Db 381 CACCTCCACGTTTGTGATCAACAATGCAAGAGTATGATGTCGCTACTCGAAGACAGCA 440  
|||  
QY 490 GACGGCTTCGAGATGCACTTTGGGTTAACCACCTGGGTCACTTCTCTTGACAACTTG 549  
|||  
Db 441 GATGGCTTTGAGATGCACATAGGAGTCAACCACTTGGGTCACTTCTCTTAACCCATCTG 500  
|||  
QY 550 CTGCTGGACAAGCTGAAAGCCTCAGCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCC 609  
|||  
Db 501 CTGCTAGAGAACTAAAGGAATCAGCCCATCAAGGATAGTAAATGTGTCTTCCCTCGCA 560  
|||  
QY 610 CATGTTGCTGGGCACATAGACTTTTGACGACTTGAACCTGGCAGACGGAAGTATAACACC 669  
|||  
Db 561 CATCACCTGGGAAGGATCCACTTCCATAACCTGCAGGGCGA---GAAATCTACAATGCA 617  
|||  
QY 670 AAAGCCGCTACTGCCAGAGCAAGCTCGCCATCGTCTCTTCAACCAAGGAGCTGAGCCGG 729  
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Db 618 GGCCTGGCCTACTGTCAAGCAAGCTAGCCCAACATCTCTTCAACCAAGGAACTGGCCCGG 677  
|||  
QY 730 CGGCTGCAAGGCTCTGGTGTGACTGTCAACGCGCTGCACCCCGGTGGCCAGGACAGAG 789  
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Db 678 AGACTAAAGGCTCTGGCGTTACGACGCTATTCTGTACACCTTGGCAGACACTCCAATCTGAA 737  
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QY 790 CTGGGCAGACACACGGGCATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCCATC 849  
|||  
Db 738 CTGGTTCGGCACTCATCTTTCATGAGATGATGT-----GGTGGCTT 779  
|||

QY 850 TTCTGGCTGCTGTCAAGAGCCCGAGCTGGCCCGCCAGCCAGCAGCAGCAGCAGCAGCAG 909  
|||  
Db 780 TTCTCCTTTTTCATCAAGACTCCTCAGCAGGAGCCAGACCCAGCAGCAGCAGCAGCAG 839  
|||  
QY 910 GCGGAGGAACCTGGCGGATGTTTCCGGAAGTACTTCGATGGACTCAAAACAGAAAGCCCG 969  
|||  
Db 840 ACAGAAGGTCTTGAGATTCTAAGTGGGAATCATTTCACTGACTGTGTCATGGCATGGTC 899  
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QY 970 GCGCCCGAGGCTGAGGATGAGGAGGTGGCGCGGAGGCTTTGGGCTGAAAGTCCCGCCTG 1029  
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Db 900 TCTGCCCAAGCTCGTAATGAGACTATAGCAAGGCGGCTGTGGACGTCAGTTGTGACCTG 959  
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QY 1030 GTGGGCTTAGAGGCTCCCTCTGTGAGGGAGCAGCCCTCCCGAGATAACCTCTCTGGAGCAG 1089  
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Db 960 CTGGGCTCCCAATAGACTAACAGGCGAGTGCCAGTTGGACCCAGAGAGACTGCAGCAG 1019  
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QY 1090 ATTTGAAAG 1098  
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Db 1020 ACTACACAG 1028  
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RESULT 6  
US-09-636-215-332  
; Sequence 332, Application US/09636215  
; Patent No. 6620922  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.42717C17  
; CURRENT APPLICATION NUMBER: US/09/636,215  
; CURRENT FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 852  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 332  
; LENGTH: 2507  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-636-215-332

Query Match 13.7%; Score 247.8; DB 4; Length 2507;  
Best Local Similarity 55.3%; Pred. No. 4.1e-49;  
Matches 536; Conservative 0; Mismatches 412; Indels 21; Gaps 2;

QY 130 GCCGCCGTGCTGTCAAGGACTATGTCACCGGTGGGCTTGGCCCGCAGCAGCCACCATC 189  
|||  
Db 81 GCTGCCCCCAATCAGGAAATGCTGTCCAGTGGGTGTGTATCATCACTGTTGAGCTT 140  
|||  
QY 190 CCTGGGAAGACGGTCACTGTCAGCGGCGCCCAACACAGGCATCGGGAAGCAGACCCCTTG 249  
|||  
Db 141 CCTGGGAAGTAGTTGTGTCACAGGAGTAAATACAGGTATCGGGAAGGAGACAGCCAAA 200  
|||  
QY 250 GAATGCGCAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 309  
|||  
Db 201 GAGTGGCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 260  
|||  
QY 310 GCGGCAAGAAAGGACATCCGCGGGGAGACCTCAATCACTGTCACCGCCCGCACCTG 369  
|||  
Db 261 TTGGTGGCAAAAGAGATCCAGACCAAGGAAACAGGAGGTGTTGGTGGCGGAACTG 320  
|||  
QY 370 GACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAGATCATTTGAAGAGGAGGAG 429  
|||  
Db 321 GACCTGCTGATCTAAGTCTATTCCAGCTTTTGCTAAGGCTTCTTAGCTGAGGAAAG 380  
|||  
QY 430 CGAGTGGACATTTCTAATCAACAAACGCGGTGTGATCGGTGCCCCCACTGGACCCAGG 489  
|||  
Db 381 CACCTCCACGTTTGTGATCAACAATGCAAGAGTATGATGTCGCTACTCGAAGACAGCA 440  
|||  
QY 490 GACGGCTTCGAGATGCACTTTGGGTTAACCACCTGGGTCACTTCTCTTGACAACTTG 549  
|||  
Db 441 GATGGCTTTGAGATGCACATAGGAGTCAACCACTTGGGTCACTTCTCTTAACCCATCTG 500  
|||  
QY 550 CTGCTGGACAAGCTGAAAGCCTCAGCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCC 609  
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Db 501 CTGCTAGAGAACTAAAGGAATCAGCCCATCAAGGATAGTAAATGTGTCTTCCCTCGCA 560  
|||  
QY 610 CATGTTGCTGGGCACATAGACTTTTGACGACTTGAACCTGGCAGACGGAAGTATAACACC 669  
|||  
Db 561 CATCACCTGGGAAGGATCCACTTCCATAACCTGCAGGGCGA---GAAATCTACAATGCA 617  
|||  
QY 670 AAAGCCGCTACTGCCAGAGCAAGCTCGCCATCGTCTCTTCAACCAAGGAGCTGAGCCGG 729  
|||  
Db 618 GGCCTGGCCTACTGTCAAGCAAGCTAGCCCAACATCTCTTCAACCAAGGAACTGGCCCGG 677  
|||  
QY 730 CGGCTGCAAGGCTCTGGTGTGACTGTCAACGCGCTGCACCCCGGTGGCCAGGACAGAG 789  
|||  
Db 678 AGACTAAAGGCTCTGGCGTTACGACGCTATTCTGTACACCTTGGCAGACACTCCAATCTGAA 737  
|||  
QY 790 CTGGGCAGACACACGGGCATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCCATC 849  
|||  
Db 738 CTGGTTCGGCACTCATCTTTCATGAGATGATGT-----GGTGGCTT 779  
|||

Db 261 TTGGTGGCCAAAGAGATCCAGACCAGCAGGGAACACGAGGTGTGGTGGGAAACTG 320  
QY 370 GACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGACGAAAGATCAATGAAGAGGAG 429  
Db 321 GACCTGTCTGATACTAAGTCTATTCGAGCTTTTGTAAAGGCTTCTTAGCTGAGGAAAG 380  
QY 430 CGAGTGGACATTTAATCAACAACGCGGGTGTGATCGGTGCCCCCACTGGACCAACGAG 489  
Db 381 CACCTCCACGTTTGTATCAACAATGCAGGAGTGATGTGTCCGTAATCGAAGACAGCA 440  
QY 490 GACGGCTTCGAGATGCAGTTTGGGGTTAAACCACTGGGTCACTTCTCTTGACAAACTTG 549  
Db 441 GATGGCTTTGAGATGCACATAGGAGTCAACCACTGGGTCACTTCTCTTAACCCATCTG 500  
QY 550 CTGCTGGACAAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCC 609  
Db 501 CTGCTAGAGAAACTAAAGGAATCAGCCCCATCAAGGATAGTAAATGTCTTCCCTCGCA 560  
QY 610 CATGTTGCTGGGCACATAGACTTTGACGACTTGAACCTGGCAGACGGAAGTATAACACC 669  
Db 561 CATCACCTGGGAAGGATCCACTTCCATAACCTGCAGGGCGA--GAAATTTCAATGCA 617  
QY 670 AAAGCCGCTACTGCCAGAGCAAGCTCGCCATCGTCTCTTCAACCAAGGAGCTGAGCCGG 729  
Db 618 GGCCTGGCCTACTGTACAGCAAGCTAGCCCAATCCTCTTCAACCCAGGAAGTGGCCCG 677  
QY 730 CGGCTGCAAGGCTCTGGTGTGACTGTCAACGCCCTGCACCCCGGCTGGCCAGGACAGAG 789  
Db 678 AGACTAAAGGCTCTGGCGTTACGACGTATTTCTGTACACCTGGCACAGTCCAATCTGAA 737  
QY 790 CTGGGCAGACACACGGGCATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCCCATC 849  
Db 738 CTGGTTCCGCACCTCATCTTTCATGAGATGGATGT-----GGTGGCTT 779  
QY 850 TTCTGGCTGTGTCAGAGCCCGGAGCTGGCCGCTGAGGAGTGAACCTTCCAGATAACCTCTGGAGCAG 1089  
Db 780 TTCTCCTTTTTCATCAAGACTCCTCAGAGGGAGCCAGACCCAGCTGCACTGTGACCTG 839  
QY 910 GCGGAGGAACCTGGCGGATGTTTCCGGAAGTACTTCGATGGAATCAACAGAGAGCCCGC 969  
Db 840 ACAGAAAGTCTTGAGATTTCAAGTGGGAATCATTTCACTGACTGTCTATGTGGCATGGGTC 899  
QY 970 GCCCCGAGGCTGAGGATGAGGAGGTGGCCCGGAGGCTTTGGGCTGAAAGTGGCCGCTG 1029  
Db 900 TCTGCCCAAGCTCGTAAATGAGACTATAGCAAGGCGGCTGTGGGACGTCACTGTGACCTG 959  
QY 1030 CTGGGCTTAGAGGCTCCCTCTGTGAGGAGCAGCCCTCCAGATAACCTCTGGAGCAG 1089  
Db 960 CTGGGCTTCCCAATAGACTAAACAGGCACTGCCAGTTGGACCCCAAGAGAGTGCAGCAG 1019  
QY 1090 ATTTGAAAG 1098  
Db 1020 ACTACACAG 1028

RESULT 7  
US-09-685-166A-332  
; Sequence 332, Application US/09685166A  
; Patent No. 6630305  
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C21  
; CURRENT APPLICATION NUMBER: US/09/685.166A  
; CURRENT FILING DATE: 2000-10-10  
; NUMBER OF SEQ ID NOS: 898  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 332  
; LENGTH: 2507  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; US-09-685-166A-332

Query Match 13.7%; Score 247.8; DB 4; Length 2507;  
Best Local Similarity 55.3%; Pred. No. 4.1e-49;  
Matches 536; Conservative 0; Mismatches 412; Indels 21; Gaps 2;

QY 130 GCGCCGCTGCTCAAGGACTATGTACCGTGGGGCTTGGCCCAAGGACCACCATC 189  
Db 81 GCTGCGCCCCAATCAGGAAATGTCTGCCAGTGGGTGTATCATCACTGTTGAGCTT 140  
QY 190 CCTGGGAAGACGGTTCATCGTACGGGGCCCAACACAGGCATCGGGAAGCAGACCGCTTG 249  
Db 141 CCTGGGAAGTAGTTGTGTGTACAGGAGCTAATACAGGTATCGGGAAGGAGACAGCCAAA 200  
QY 250 GAACTGGCCAGGAGGAGGCAACATCATCTTGGCCTGCCGAGACATGGAAGAGTGTGAG 309  
Db 201 GAGCTGGCTCAGAGAGGAGCTCGAGTATATTAGCTTGGGGATGTGGAAGGGGGAA 260  
QY 310 GCGGCAGCAAGGACATCCGGGGGAGACCCCTCAATCACCATGTCAACGCCCGGCACCTG 369  
Db 261 TTGGTGGCCAAAGAGATCCAGACCACGACAGGGAACCCAGCAGGTGTGGTGGGAACTG 320  
QY 370 GACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTCAGCAAAAGATCATTTGAAGAGGAGGAG 429  
Db 321 GACTGTCTGATACTAAGTCTATTTCGAGCTTTTCTAAGGGCTTCTTAGTGTGAGGAAAG 380  
QY 430 CGAGTGGACATTTCTAATCAACAACGCGGGTGTGATCGGGTGGCCCACTGGACCCAGCAG 489  
Db 381 CACCTCCACGTTTGTATCAACAATGCAGGAGTGTATGTGTCCGTACTCGAAGACAGCA 440  
QY 490 GACGGCTTCGAGATGCAGTTTGGCGTTAAACCACTGGGTCACTTCTCTTGACAAACTTG 549  
Db 441 GATGGCTTTGAGATGCACATAGGAGTCAACCACTTGGGTCACTTCTCTTAACCCATCTG 500  
QY 550 CTGCTGGACAAGCTGAAAGCCTCAGCCCTTCCGCGATCATCAACCTCTCGTCCCTGGCC 609  
Db 501 CTGCTAGAGAAACTAAAGGAATCAGCCCCATCAAGGATAGTAAATGTCTTCCCTCGCA 560  
QY 610 CATGTTGCTGGGCACATAGACTTTGACGACTTGAACCTGGCAGACGGAAGTATAACACC 669  
Db 561 CATCACCTGGGAAGGATCCACTTCCATAACCTGCAGGGCGA---GAAATTTCAATGCA 617  
QY 670 AAAGCCGCTACTGCCAGAGCAAGCTCGCCATCGTCTCTTCAACCAAGGAGTGCAGCCGG 729  
Db 618 GGCCTGGCCTACTGTACAGCAAGCTAGCCCAACATCCTCTTCAACCCAGGAAGTGGCCCG 677  
QY 730 CGGCTGCAAGGCTCTGGTGTGACTGTCAACGCCCTGCACCCCGGCTGGCCAGGACAGAG 789  
Db 678 AGACTAAAGGCTCTGGCGTTACGACGTATTTCTGTACACCTGGCACAGTCCAATCTGAA 737  
QY 790 CTGGGCAGACACACGGGCATCCATGGCTCCACCTTCTCCAGCACCACTCGGGGCCCATC 849  
Db 738 CTGGTTCCGCACCTCATCTTTCATGAGATGGATGT-----GGTGGCTT 779  
QY 850 TTCTGGCTGTGTCAGAGCCCGGAGCTGGCCGCTGAGGAGTGAACCTTCCAGATAACCTCTGGAGCAG 909  
Db 780 TTCTCCTTTTTCATCAAGACTCCTCAGAGGGAGCCAGACCCAGCTGCACTGTGACCTTA 839











RESULT 12  
PCT-US95-01827A-1  
; Sequence 1, Application PC/TUS9501827A  
; GENERAL INFORMATION:  
; APPLICANT: HE, ET AL.  
; TITLE OF INVENTION: Human Prostatic Specific Reductase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELIA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/01827A  
; FILING DATE: Concurrently  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FERRARO, GREGORY D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 325800-228  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1086 BASE PAIRS  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: SINGLE  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: cDNA  
PCT-US95-01827A-1

Query Match 12.9%; Score 233.2; DB 5; Length 1086;  
Best Local Similarity 55.8%; Pred. No. 8.7e-46;  
Matches 498; Conservative 0; Mismatches 373; Indels 21; Gaps 2;  
  
QY 130 GCCGCCGTGCTCAAGGACTATGTACCGGTGGGCTTGCCCGCAGCAAGGCCACCATC 189  
|||  
Dd 67 GCTGCGCCCCAAATCAGGAAATGCTGTCAGTGGGTGTGATCATCAACTGTTTCAGCTT 126  
|||  
  
QY 190 CCTGGGAAGACGGTCATCGTGACGGGGCCCAACACAGGCATCGGGAAGCAGACCGCCCTTG 249  
|||  
Dd 127 CCTGGGAAAGTAGTTGTGTCACAGGAGCTAATACAGGTATCGGGAAGGAGACAGCCAAA 186  
|||  
  
QY 250 GAACTGGCCAGAGAGAGGCAACATCATCTGGCCTGCCGAGACATGGAGAAGTGTGAG 309  
|||  
Dd 187 GAGCTGGCTCAGAGAGGAGCTCGAGTATATTAGCTTGCCGGGATGTGGAAAAGGGGAA 246  
|||  
  
QY 310 GCGGCAGCAAGGACATCCGCGGGGAGACCTCAATCACCATGTCAACGCCCGCACCTG 369  
|||  
Dd 247 TTGGTGGCCAAAGAGATCCAGACCAGAGGGAAACCAGCAGGTGTTGGTTCGGAAACTG 306  
|||  
  
QY 370 GACTTGGCTTCCCTCAAGTCTATCCGAGAGTTGCAGCAAAAGATCATTTGAAGAGGAGG 429  
|||  
Dd 307 GACCTGTCTGATACTAAGTCTATTTCGAGCTTGGGCTAAGGGCTTCTTAGCTGAGGAAAAG 366  
|||  
  
QY 430 CGAGTGGACATTCTAATCAACAACGCGGGGTGTGATCGGGTGCCCGCACTGGACCCAGG 489  
|||  
Dd 367 CACCTCCACGTTTGGATCAACAATGCAGGAGTATGATGTGTCCTACTCGAAGACAGCA 426  
|||  
  
QY 490 GACGGCTTCGAGATGCAGTTTGGCGTTAACACCTGGGTCACTTCTCTTGACAAACTTG 549  
|||

Db 427 GATGGCTTTGAGATGCACATAGGAGTCAACCACATTGGGTCACTTCTCTTAACCCATCTG 486  
  
QY 550 CTGCTGGACAAGCTGAAAGCCTCAGCCCTTCGGGATCATCAACTCTCTGTCCTCGGCC 609  
|||  
Dd 487 CTGCTAGAGAAACTAAAGGAATCAGCCCATCAAGGATAGTAAATGTCTTCCCTCGCA 546  
|||  
  
QY 610 CATGTTGCTGGGCACATAGACTTTGACGACTTGAACCTGGCAGAGGAGGAATATAACACC 669  
|||  
Dd 547 CATCACCTGGGAAGGATCCACTTCCATAACCTGCAGGGCGA---GAAATCTACRAATGCA 603  
|||  
  
QY 670 AAAGCCGCTACTCCAGAGCAAGCTCGCCCATCGTCTCTTCAACAAGGAGCTGAGCCGG 729  
|||  
Dd 604 GGCCTGGCCTACTGTACAGCAAGCTAGCAACATCTCTTCAACCAGGAACCTGGCCCGG 663  
|||  
  
QY 730 CGGCTGCAAGSCTCTGGTGTGACTGTCAACGCCCTTGCAACCCCGCGTGGCCAGGACAGAG 789  
|||  
Dd 664 AGACTAAAGSCTCTGGCGTTACGCGTATTCTGTACACCCCTGSCACAGTCCAATCTGAA 723  
|||  
  
QY 790 CTGGGCAGACACACGGGCATCCATGCTCCACCTTCTCCAGCACACACACTCGGGCCCATC 849  
|||  
Dd 724 CTGGTTCGGCACTCATCTTTTCATGAGATGA-----TGTGGTGGCTT 765  
|||  
  
QY 850 TTCTGGCTGCTGGTCAAGAGCCCCGAGCTGGCCGCCAGCCCGACACATACCTGGCCCGTG 909  
|||  
Dd 766 TTCTCCTTTTTCATCAAGACTCCTCAGCAGGGAGCCAGACCAGGCTGCACTGTGCCCTTA 825  
|||  
  
QY 910 GCGGAGGAACCTGGCGGATGTTTCCGGAAGTACTTTCGATGGACTCAAAACAGAAGGCCCG 969  
|||  
Dd 826 ACAGAAGGCTTGAGATTCTAAGTGGGAATCATTTTCAGTACTGTGATGTCATGTCGTCATG 885  
|||  
  
QY 970 GCCCCGAGGCTGAGGATGAGGAGGTGGCCCGGAGGGCTTTGGGCTGAAAGTG 1021  
|||  
Dd 886 TCTGCCCAAGCTCGTAATGAGACTATAGCAAGGCGGCTGTGGGACGTCATTG 937  
|||

RESULT 13  
US-09-833-381-933  
; Sequence 933, Application US/09833381  
; Patent No. 6672186  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs  
; FILE REFERENCE: 5800-119  
; CURRENT APPLICATION NUMBER: US/09/833,381  
; CURRENT FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: 09/516,448  
; PRIOR FILING DATE: 2000-02-29  
; NUMBER OF SEQ ID NOS: 2050  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 933  
; LENGTH: 234  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-833-381-933

Query Match 12.1%; Score 219.6; DB 4; Length 234;  
Best Local Similarity 96.2%; Pred. No. 8.7e-43;  
Matches 225; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
  
QY 1184 GCGGCCGCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGAGTGGACTGGCCTG 1243  
|||  
Dd 1 GCGGCCGCATGCCCGCAGTACGTTCTAGGGGGCGGTGCTGGCCGAGTGGACTGGACTG 60  
|||  
  
QY 1244 CAGGTGAGCACTGCCCCGGGCTCTGGCTGGTTCGGTCTGCTCTGCTGCCAGAGGGGAGA 1303  
|||  
Dd 61 CAGGTGAGCACTGCCCCTGGGCTCTGGCTGGTTCGGTCTGCTCTGCTGCCATCAAGGGAGA 120  
|||  
  
QY 1304 GGGGCCATCTGATGCTTCCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAGGGCT 1363  
|||  
Dd 121 GGGGCCATCTGATGCTTCCCCTGCGAATCTAAACTGGTAATGGCCGAGGAGGAGGGCT 180  
|||  
  
QY 1364 CTGTGCACTTGACAGCCACGTGAGGAGAGCCGCGGTGCTGTCGGGAGGGGTT 1417  
|||

Db 181 CCGTGCACTTGAGGCGACGTCAGGAGAGCCAGCGGTGCCCTGTGCGGGAGGGTT 234

RESULT 14

US-09-103-840A-2

; Sequence 2, Application US/09103840A

; Patent No. 6294328

; GENERAL INFORMATION:

; APPLICANT: FLEISCHMAN, Robert D.

; APPLICANT: WHITE, Owen R.

; APPLICANT: FRASER, Claire M.

; APPLICANT: VENTER, John C.

; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

; FILE REFERENCE: 24366-20007.00

; CURRENT APPLICATION NUMBER: US/09/103.840A

; CURRENT FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 4403765

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

; FEATURE:

; OTHER INFORMATION: CDC 1551

; OTHER INFORMATION: "n" bases at various positions throughout the sequence

; OTHER INFORMATION: represent a, t, c or g

US-09-103-840A-2

Query Match 9.3%; Score 168.2; DB 3; Length 4403765;

Best Local Similarity 54.7%; Pred. No. 2.2e-29;

Matches 357; Conservative 0; Mismatches 293; Indels 3; Gaps. 1;

QY 155 TCACCGGTGGGGTTGCCCCAGCAAGGCCACCATCCCTGGGAGACGGTCACTCGTGACGG 214

Db 75279 TGACCAAATGGACTGCCGCCGACATTCTGTACCAGACCGCGCGGACCGCGTCAACGG 75338

QY 215 GCGCCAAACACAGGCATCGGGAAGCAGACCGCCTTGGAACTGGCCAGGAGAGGCAACA 274

Db 75339 GGGCCAAACACCGGACTTGGATTTCGAGACCGCGCAGCGCTTGCCGCCCATGGTGCACACG 75398

QY 275 TCATCCTGGCCTGCCGAGACATGGAGAAGTGTGAGGCGGCAGCAAAAGGACATCCGCGGG 334

Db 75399 TGGTGTGGCTGTGCGCAACCTCGACAAGGCAAGCAGCGGCGGCACGCATCACCGAGG 75458

QY 335 AGACCCCTCAATCACCATGTCAACGCCCGCACCTTGGACTTGGCTTCCCTCAAGTCTATCC 394

Db 75459 CCACCCCGCGCGCGAAGTAGAGCTTCAGAGACTTGACCTGACTCGCTGGCGTGGTGC 75518

QY 395 GAGAGTTTGCAGAAAGATCATTTGAAGAGAGGAGCGAGTGGACATTCTAATCAACAACG 454

Db 75519 GCGCGCGCGCGCACAGCTGAAGTCTGACCAACGCGCATCGACTGCTGATCAACAACG 75578

QY 455 CGGGTGTGATGCGGTGCCCCACTGGACCAACCGAGGACGGCTTCGAGATGCAGTTTGGCG 514

Db 75579 CCGGGTGTATATACACCCCGACAGACCAACAGCAGACGGCTTCGAGATGCAGTTCGGCA 75638

QY 515 TTAACCACTGGGTCACTTTCTCTTGACAAACTTGTCTGCTGGCAAGCTGAAAGCCTCAG 574

Db 75639 CCAACCACTTGGGCCATTTGCGGTTGACCGGCTGTTGATTGATCGACTGCTGCCCGTCG 75698

QY 575 CCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGGGCACATAGACTTG 634

Db 75699 CCGGTTACAGAGTGGTCACCATCAGCAGCGTCGGCCATCGCATCCGTGCCGAATCCATT 75758

QY 635 ACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAGCCGCCCTACTGCCAGAGCAAGC 694

Db 75759 TCGACGACCTCCAGTGGGAACGCCGGTACAGCGGGTCCGCCCTACGGCCAAAGCCAAGC 75818

QY 695 TCGCCATCGTCTCTTACCAAGGAGCTGAGCCGGCGGTGCAAGGCTCTGGTGTGACTG 754

Db 75819 TCGCCAACTGTCTTCACTTATGAACCTTCAGCGTGGTTAGCACCGGGCGGAACCAACA 75878

QY 755 TC---AACGCCCTGCACCCCGCGTGGCCAGGACAGAGCTGGGCAGACACACG 804

Db 75879 TCGCGGTGCGGTGCGCACCCCGGAGTGTCCAACACCGAACTGGTCCGCAACATG 75931

RESULT 15

US-09-103-840A-1

; Sequence 1, Application US/09103840A

; Patent No. 6294328

; GENERAL INFORMATION:

; APPLICANT: FLEISCHMAN, Robert D.

; APPLICANT: WHITE, Owen R.

; APPLICANT: FRASER, Claire M.

; APPLICANT: VENTER, John C.

; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

; FILE REFERENCE: 24366-20007.00

; CURRENT APPLICATION NUMBER: US/09/103.840A

; CURRENT FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 4411529

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

; OTHER INFORMATION: H37Rv

US-09-103-840A-1

Query Match 9.2%; Score 166.6; DB 3; Length 4411529;

Best Local Similarity 54.5%; Pred. No. 5.4e-29;

Matches 356; Conservative 0; Mismatches 294; Indels 3; Gaps 1;

QY 155 TCACCGGTGGGCTTGCCCCAGCAAGGCCACCATCCCTGGGAAGACGGTCACTCGTGACGG 214

Db 75300 TGACCAAATGGACTGCCGCCGACATTCTGTACCAGACCGCGCGGACCGCGTCAACGG 75359

QY 215 GCGCCAAACACAGGCATCGGGAAGCAGACCGCCTTGGAACTGGCCAGGAGAGGCAACA 274

Db 75360 GGGCCAAACACCGGACTTGGATTTCGAGACCGCGCAGCGCTTGCCGCCCATGGTGCACACG 75419

QY 275 TCATCCTGGCCTGCCGAGACATGGAGAAGTGTGAGGCGGCAGCAAAAGGACATCCGCGGG 334

Db 75420 TGGTGTGGCTGTGCGCAACCTCGACAAGGGCAAGCAGCGCGCGGCACGCATCACCGAGG 75479

QY 335 AGACCCCTCAATCACCATGTCAACGCCCGGCACCTTGGACTTGGCTTCCCTCAAGTCTATCC 394

Db 75480 CCACCCCGCGCGCGAAGTAGAGCTTCAGAGACTTGACCTGACTCGCTGGCGTGGTGC 75539

QY 395 GAGAGTTTGCAGCAAAAGATCATTTGAAGAGGAGGAGCGAGTGGACATTCTAATCAACAACG 454

Db 75540 GCGCGCGCGCGCACAGCTGAAGTCTGACCAACGCGCATCGACTGCTGATCAACAACG 75599

QY 455 CGGGTGTGATGCGGTGCCCCACTGGACCAACCGAGGACGGCTTCGAGATGCAGTTTGGCG 514

Db 75600 CCGGGTGTATATACACCCCGACAGACCAACAGCAGACGGCTTCGAGATGCAGTTCGGCA 75659

QY 515 TTAACCACTGGGTCACTTTCTCTTGACAAACTTGTCTGCTGGCAAGCTGAAAAGCCTCAG 574

Db 75660 CCAACCACTTGGGCCATTTGCGGTTGACCGGCTGTTGATTGATCGACTGCTGCCCGTCG 75719

QY 575 CCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGGGCACATAGACTTTG 634

Db 75720 CCGGTTACAGAGTGGTCACCATCAGCAGCGTCGGCCATCGCATCCGTGCCGAATCCATT 75779

QY 635 ACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAGCCGCCCTACTGCCAGAGCAAGC 694

Db 75780 TCGACGACCTCCAGTGGGAACGCCGGTACAGCGGGTCCGCCCTACGGCCAAAGCCAAGC 75839

QY 695 TCGCCATCGTCTCTTACCAAGGAGCTGAGCCGGCGGTGCAAGGCTCTGGTGTGACTG 754

Db 75840 TCGCCAACTGTCTTCACTTATGAACCTTCAGCGTGGTTAGCACCGGGCGGAACCAACA 75899

QY 755 TC---AACGCCCTGCACCCCGCGTGGCCAGGACAGAGCTGGGCAGACACACG 804

Db 75900 TCGCGGTGGGTGGCACC CGGGAGTGTCCAACACCGAAGTGGTCCGCAACATG 75952

Search completed: June 23, 2004, 14:47:06  
Job time : 160 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 23, 2004, 11:04:49 ; Search time 21 Seconds  
(without alignments)  
1516.162 Million cell updates/sec

Title: US-10-015-393A-116  
Perfect score: 1695  
Sequence: 1 MSRYLLPLSALGTVAGAAVL.....ESARLVGLEAPSVREQPLPR 331

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	566	33.4	303	2 E70848	probable oxidoredu
2	534	31.5	311	2 H70829	hypothetical prote
3	531.5	31.4	304	2 T44727	probable oxidoredu
4	515	30.4	320	2 S42651	hypothetical prote
5	513.5	30.3	336	2 H75255	oxidoreductase, sh
6	497	29.3	321	2 T02520	probable oxidoredu
7	487.5	28.8	350	2 T48275	hypothetical prote
8	485.5	28.6	311	2 AD2021	hypothetical prote
9	485	28.6	323	2 E87298	hypothetical prote
10	475.5	28.1	317	2 C70863	hypothetical prote
11	457.5	27.0	316	2 D84206	probable oxidoredu
12	456	26.9	317	2 T10561	hypothetical prote
13	451	26.6	309	2 C83017	probable short cha
14	447.5	26.4	332	2 T13447	hypothetical prote
15	438.5	25.9	301	2 AE3195	dehydrogenase Atu5
16	437	25.8	333	2 T19314	hypothetical prote
17	428	25.3	339	2 T41570	hypothetical prote
18	414	24.4	311	2 T37155	probable oxidoredu
19	402	23.7	312	2 T37150	probable oxidoredu
20	390.5	23.0	294	2 T05381	hypothetical prote
21	382.5	22.6	204	2 T46363	hypothetical prote
22	381	22.5	400	2 C75365	daunorubicin C-13
23	364	21.5	329	2 AI2023	probable oxidoredu
24	362.5	21.4	312	2 D83689	hypothetical prote
25	357	21.1	297	2 S19842	probable oxidoredu
26	356	21.0	397	2 S71468	probable oxidoredu
27	353.5	20.9	298	2 A47089	probable oxidoredu
28	349.5	20.6	291	2 G97327	short-chain alcoho
29	345.5	20.4	400	2 S20941	protochlorophyllid

30	345	20.4	339	2 B86906	oxidoreductase yxd
31	342	20.2	388	2 S04783	protochlorophyllid
32	342	20.2	398	2 T33973	hypothetical prote
33	341.5	20.1	296	2 D82515	ketoreductase XF27
34	339	20.0	388	2 S39394	protochlorophyllid
35	338.5	20.0	401	2 T08936	protochlorophyllid
36	338	19.9	398	2 JC4146	protochlorophyllid
37	336	19.8	322	2 T43931	protochlorophyllid
38	336	19.8	329	2 T15910	hypothetical prote
39	331	19.5	313	2 S08406	protochlorophyllid
40	329	19.4	401	2 T00897	protochlorophyllid
41	328.5	19.4	400	2 S30167	protochlorophyllid
42	326.5	19.3	395	2 S52285	NADPH2 dehydrogena
43	325	19.2	322	2 S76636	hypothetical prote
44	317.5	18.7	322	2 T04022	hypothetical prote
45	312	18.4	302	2 H70523	hypothetical prote

ALIGNMENTS

RESULT 1  
E70848  
probable oxidoreductase - Mycobacterium tuberculosis (strain H37RV)  
C;Species: Mycobacterium tuberculosis  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
C;Accession: E70848  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, J.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998  
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom  
A;Reference number: A70500; MUID:98295987; PMID:9634230  
A;Accession: E70848  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-303 <COL>  
A;Cross-references: GB:AL021428; GB:AL123456; NID:g3261514; PIDN:CAA16249.1; PID:g2808  
A;Experimental source: strain H37RV  
C;Genetics:  
C;Gene: RV0068  
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
F;15-208/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match	33.4%;	Score 566;	DB 2;	Length 303;
Best Local Similarity	43.9%;	Pred. No. 1.3e-37;		
Matches 133;	Conservative 47;	Mismatches 101;	Indels 22;	Gaps 8;
QY	34	ATIP---GKTVIVTGANTGIGKQTALALEARRGGNIILACRDMKCEAAAKDIRGETLNHH	90	
Db	7	ADIPDQTGRTAVITGANTGLGFETAALAAHGAHVLAVRNLDKGKQAAARITEATPGAE	66	
QY	91	VNARHLDLASLKSIREFAAKIIEEERVDILINNAGVMRCPHWTTEDGFEMQFVGNHLGH	150	
Db	67	VELQELDLTSLASVRAAAQQLKSDHQRIIDLLINNAGVMYTPRQTADGFEMQFGTNHLGH	126	
QY	151	FLLTNLLLDKLKASAPSRRIINLSSLAH-VAGHIDFDDLNWQTRKYNTKAAYCOSKLAIVL	209	
Db	127	FALTGLLLIDRLLPVAGSRVVTISSVGHRIIRAAIHFDLQWE-RRYRVRVAAAYGQAKLANLL	185	
QY	210	FTKELSRRLQSGVTVN-ALHPGVARTELGRHTGIHGSTFSSTTLGPIFWLLVKSPELAA	268	
Db	186	FTYELQRLAPGGTTIAVASHPGVSNTFV-----VRNMPRPLVAVAAILAPLMQDAELGA	240	
QY	269	QPSTYLAVAEELADVSGKYF--DGL-----KQKAPAPEAEDEEVARRLWAESARLVGL	319	
Db	241	LPT--LRAATDPAVRGGQYFGPDGFGFGEIRGYPKVVASSAQSHDEQLQRLWAVSEELTV	298	
QY	320	EAP	322	
Db	299	VYP	301	

RESULT 2  
H70829  
hypothetical protein Rv0439c - Mycobacterium tuberculosis (strain H37RV)  
C/Species: Mycobacterium tuberculosis  
C/Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
C/Accession: H70829  
R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998  
A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A/Reference number: A70500; MUID:98295987; PMID:9634230  
A/Accession: H70829  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-311 <COL>  
A/Cross-references: GB:AL021932; GB:AL123456; NID:g3261527; PIDN:CAA17396.1; PID:g290951  
A/Experimental source: strain H37RV  
C/Genetics:  
C/Gene: Rv0439c  
C/Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
F/22-216/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match	31.5%;	Score 534;	DB 2;	Length 311;
Best Local Similarity	43.3%;	Pred. No. 4.9e-35;		
Matches 132;	Conservative 42;	Mismatches 105;	Indels 26;	Gaps 10;

  

QY	32	SKATIP---GKTIVITGANTGIGKQFALELARRGGNIILACRDMEKCEAAAKDIRGETLN	88
		:   :                     :   :   :	
Db	12	SAADVDPQSGRVVVTGANTGIGYHTAAVFADRGAHVVLAVRNLEKGNAAARARIMAARPG	71
		:   :                     :   :   :	
QY	89	HHVNARHLDLASLKSIREFAAKIIEBERVDILINNAGVMRCPHWTTEDGFEMQFGVNH	148
		:               :   :   :	
Db	72	AHVTLQQLDCLSDSVRAAADALRTAYPRIDVLINNAGVMVTPKQVTKDGFELQFGT	131
		:               :   :   :	
QY	149	GHFLLTNLLDLKASAPSRRIINLSSLAH-VAGHIDFDDLINWQTRKYNTKAAVCQSKLAI	207
		:   :   :   :   :   :   :   :   :   :	
Db	132	GHFALTGLVDHMLPVPGSRVTVTVSSQGHRIHAAIHFDLQWE-RRYNRVAAAYGOAKLAN	190
		:   :   :   :   :   :   :	
QY	208	VLFTKELSRRL--QGSGVTVNALHPGVARTELGRHTG--IHGSTFSSITLGPFWLLVKS	263
		:                     :         :   :	
Db	191	LLFTYELQRLGEAGKSTIAVAHPGGSNTLTRLNPLRLRP---VATVLGP---LLFQS	244
		:   :   :   :   :   :   :	
QY	264	PELAAQPSITYLVAEELADVSGKYF--DCLKQKAPAP-----EADEEVARRLWAESA	314
		:       :   :   :   :   :   :   :   :   :	
Db	245	PEMGALPT--LRAATDPTTQGGQYYGPDGFGEQRGHPKVVSQAQSHDKDLQRLWTVSE	302
		:       :   :   :   :   :   :   :   :   :	
QY	315	RLVGL	319
		:	
Db	303	ELTGV	307

RESULT 3  
T44727  
probable oxidoreductase [imported] - Mycobacterium leprae  
C;Species: Mycobacterium leprae  
C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 04-Mar-2000  
C;Accession: T44727  
R;James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, January 1998  
A;Reference number: Z22831  
A;Accession: T44727  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-304 <JAM>  
A;Cross-references: EMBL:AL035159; PIDN:CAA22691.1  
A;Experimental source: cosmid B1450  
C;Genetics:  
A;Note: MLCB1450.07  
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match	31.4%;	Score	531.5;	DB	2;	Length	304;
Best Local Similarity	43.0%;	Pred. No.	7.5e-35;				
Matches	132;	Conservative	45;	Mismatches	101;	Indels	29;
						Gaps	10;

  

QY	34	ATIP---	GKTIVITGANTGIGKQTAL	ELARRGGNIILACRDM	KECAA	KDIRGETLNHH	90
			: :         :	: :         :	: :         :	: :         :	:
Db	7	ADIPDQ	GRVAVITGANTGLGYQTAL	ALAEHGAHVVLAVRNL	DKGDA	AARITATSAQNN	66
			: :         :	: :         :	: :         :	: :         :	:
QY	91	VNARHL	DLASLKSIREFAAKII	EEERVDILINNAGVM	RCPHWTT	EDGFEMQFGVNH	150
			:         :	:         :	:         :	:         :	:
Db	67	VALQEL	DLASLESVRAAAKQL	RSYDHYDIDLINNAG	VWMTPKSTTK	DGFELQFGTNH	126
			:         :	:         :	:         :	:         :	:
QY	151	FLLTNLL	LDKLKASAPSR	IINLSSLAH-VAGH	IDFDDL	NWQTRKYN	209
			:         :	:         :	:         :	:         :	:
Db	127	FAFTGL	LLDRLLPIVGS	RVTVSSLSHRL	FADHFNDLQ	WEC-NYNR	185
			:         :	:         :	:         :	:         :	:
QY	210	FTKELSR	RRLQSGWTVN-AL	HPGVART	ELGRHTGIHGS	TFSS	264
			:         :	:         :	:         :	:         :	:
Db	186	FTYELQ	RRLATQTTIA	VAAPGGS	RTELT	TL-----	237
			:         :	:         :	:         :	:         :	:
QY	265	ELAAQ	PSTYLVA	AEELADV	SGKYF--DGL	KQ-----	315
			:   :   :	:   :   :	:   :   :	:   :   :	:
Db	238	ATGALPT--	LRAATDA	AVLGGQY	FGPDGFAE	IRGHFKV	295
			:   :   :	:   :   :	:   :   :	:   :   :	:
QY	316	LVGLEAP	322				
			:   :   :	:   :   :	:   :   :	:   :   :	:
Db	296	LTGVVYP	302				
			:   :   :	:   :   :	:   :   :	:   :   :	:

RESULT 4  
S42651  
hypothetical protein - rape  
C/Species: Brassica napus (rape)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jul-2000  
C/Accession: S42651  
R/Coupe, S.A.; Taylor, J.E.; Isaac, P.G.; Roberts, J.A.  
Plant Mol. Biol. 24, 223-227, 1994  
A/Title: Characterization of a mRNA that accumulates during development of oils  
A/Reference number: S42651; MUID:94154236; PMID:8111020  
A/Accession: S42651  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-320 <OU>  
A/Cross-references: EMBL:X74225; NID:g456719; PIDN:CAB58175.1; PID:g6065752  
C/Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homolog  
F:34-235/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match	30.4%;	Score 515;	DB 2;	Length 320;		
Best Local Similarity	42.8%;	Pred. No. 1.7e-33;				
Matches 125;	Conservative 50;	Mismatches 93;	Indels 24;	Gaps 8;		
QY	40	TVIVTGANTGIGKQTAL	ELARRGGNIILACRDM	KECEAAAKDIRGETLNHHV	NAR-----H	95
DB	35	TAIITGGTSGIGLEAAR	VLGMRGAHVIIASRNTK	----AANDSKEMILQMP	NARIDCLQ	90
QY	96	LDLASLKSIREPAAKI	IEEERVDILINNAGVM	RCPHWTTE	DGFEMQFGVNHIGHFL	LTN 155
DB	91	LDLSSIKSVRSFIHQF	ALNVPLNILINNAGVM	FCFQLSE	DGIESQFATNHIGHFL	LTN 150
QY	156	LLLDKLIKASA-----	PSRIINLSSLAHVAGH	---IDFDDL	NWQTRKYNTKAAYCQ	SKLAI 207
DB	151	LLLDKMKSSARESGIE	GRIVNLSSIAHTYTYT	EGIMFDYIN-DPDRY	SEKKAYGQSKLAN	209
QY	208	VLFTKELSRRLQSGV--	TVNALHPGVARTELGR	HTGIHGSTFS	STTLGPIFWLLVKS	PE 265
DB	210	LLHSNALSRKLQEEGV	NITINSVHPGLITTNL	FRHSGLGMAVLKAMS	----FFLWKNI	PQ 265
QY	266	LAAQPSPTYLAVAEEL	ADVSGKYFDGLKQKAP	EADEEVARRLWAES	ARLV	317
DB	266	GAA--TTCYVALHPDL	KDVTGKYFADCNVTT	PSNFATDTTLADKL	WDPSIKLV	316

## RESULT 5







QY 136 EDGFEMQFGVNHGLHFLTNLLDKLKASAPSRILNSSLAHVAGHIDFDDLNWQTRKYN 195  
Db 113 ADGPELOFGSNHGLHFALTAAHLLPLLRAAQARVVSLSLAARRGRIHPDDLQFE-RSYA 171  
QY 196 TKAAYCQSKLAIVLFTKELSRRLQ--GSGVTVNALHPGVARTELGRHTGTHGST----- 247  
Db 172 PMTAYGQSKLAVLMPARELDRRSRAAGWGIISNAHPGLTKTNLQIAGPSHGRDKPALME 231  
QY 248 ---FSSTTLGPIFWLLVKSPELAAQSPSTYLAVAEIADVSGKYF-----DGLKQ- 293  
Db 232 RLYKTSWRFPFLWQEIIEGIL---PALY-AAATPOAD-GGAFYGRGRYEVAGGGVREA 286  
QY 294 KAPAPEAEDEEVARRLWAESARLVGLEAPSVR 325  
Db 287 KVPAAARNAD-SKRLWEVSEQLTGVSYPKSR 317

RESULT 11  
D84206  
probable oxidoreductase [imported] - Halobacterium sp. NRC-1  
C;Species: Halobacterium sp. NRC-1  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 16-Feb-2001  
C;Accession: D84206  
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;  
Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon  
Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li  
A;Title: Genome sequence of Halobacterium species NRC-1.  
A;Reference number: A84160; MUID:20504483; PMID:11016950  
A;Accession: D84206  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-316 <STO>  
A;Cross-references: GB:AE004437; NID:G10580084; PIDN:AAG19016.1; GSPDB:GN00138  
C;Genetics:  
A;Gene: yajO1  
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 27.0%; Score 457.5; DB 2; Length 316;  
Best Local Similarity 38.6%; Pred. No. 6.4e-29;  
Matches 120; Conservative 43; Mismatches 129; Indels 19; Gaps 8;  
QY 23 DIVTGGACPSKATIPGKTVIVTGANTGIGKQTALALEARRGGNIILACRDMKCEAAAKDI 82  
Db 5 DAWTAALPDQS---GRRVVVTGANSGLGFEATRAFARAGAHVVMACRSTERGEDARDI 61  
QY 83 RGETLNHHVNARHLDLASLKSIREFAAKIIEEERVDILINNAGVMRCPHWTTEDEGPEMQ 142  
Db 62 VAELPGASLTVHELDLAALDSVAAFADWFTAEFDSLHLVLANNAGVMAIPRSETADGFETQ 121  
QY 143 FGVNHLGHFLTNLLDKL-KASAPSRILNSSLAHVAGHIDFDDLNWQTRKYNTKAAYC 201  
Db 122 FGVNHLGHVALTAGLLGLVLRRTSGETRVVVTQSSGAHRRGRIDFEDLQHEA-EYGKWEAYS 180  
QY 202 QSKLAIVLFTKELSRRLQSGVTVN--ALHPGVARTELG-RHTGIHGSTFFSSTTLGPIFW 258  
Db 181 QSKLANLLFAYELDRRLRAASASVTSVACHFGYAATNLQLRGPQAAGSRLLRLAMRAANA 240  
QY 259 LLVKSPELAAQSPSTYLAVAEELADVSGKYF--DGL-----KQKAPAPEAEDEEVARRL 309  
Db 241 LVGQSAEQGAWPLLYAATNPSID--CGEYICGPGVLMRMRGHPERQOPSARSRDEDTARRL 298  
QY 310 WAESARLVGLE 320  
Db 299 WTVSADRTGVD 309

RESULT 12  
T10561  
hypothetical protein F25E4.30 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 04-Mar-2000  
C;Accession: T10561  
R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancro  
submitted to the Protein Sequence Database, June 1999  
A;Reference number: Z16533  
A;Accession: T10561  
A;Molecule type: DNA  
A;Residues: 1-317 <BEV>  
A;Cross-references: EMBL:AL050399; GSPDB:GN00062; ATSP:F25E4.30  
A;Experimental source: cultivar Columbia; BAC clone F25E4  
C;Genetics:

A;Map position: 4  
A;Introns: 36/1; 113/2; 140/1; 191/2; 217/3; 246/1; 261/3  
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
Query Match 26.9%; Score 456; DB 2; Length 317;  
Best Local Similarity 37.2%; Pred. No. 8.4e-29;  
Matches 109; Conservative 56; Mismatches 112; Indels 16; Gaps 5;

QY 38 GKTIVITGANTGIGKQTALALEARRGGNIILACRDMKCEAAAKDIRGETLNHHVNARHLD 97  
Db 29 GLTAIVTGASSGIGEETTRVLALRGVHVMAVRNTDSGNQVRDKILKEIPQAKIDVMKLD 88  
QY 98 LASLKSIREFAAKIIEEERVDILINNAGVMRCPHWTTEDEGPEMQFGVNHLGHFLTNLL 157  
Db 89 LSSMASVRSFASEYQSLDLPNLILINNAGIMACPFLLSSDNIELQFATNHLGHFLTNLL 148  
QY 158 LDKLKASA-----PSRIINLSSLAHVAGH---IDFDDLNWQTRKYNTKAAYCQSKLAIVL 209  
Db 149 LERMKKTASESNREGRIIVVSSEGRFAYREGVQFDKINDEAR-YNTLQAYGQSKLGNIL 207  
QY 210 FTKELSR--RLQSGVTVNALHPGVARTELGRTHTGTHGSTTTLGPIFWLLVKSPELA 267  
Db 208 HATELARLFKEQGVNITANSLHPSIMTNLLRY-----HSFINTIGNAVGKYLKSIPOG 262  
QY 268 AQPSTYLAVAEELADVSGKYFDGLKQKAPAPEAEDEEVARRLWAESARLVGLE 320  
Db 263 AATTCTAALHPQAKGVSGEYLMNDNNISDPNSQGDKDLAKKLWFEFSRLTSEE 315

RESULT 13  
C83017  
probable short chain dehydrogenase PA5031 [imported] - Pseudomonas aeruginosa (strain P  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C;Accession: C83017  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: C83017  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-309 <STO>  
A;Cross-references: GB:AE004916; GB:AE004091; NID:g9951315; PIDN:AAG08416.1; GSPDB:GN00  
A;Experimental source: strain PA01  
C;Genetics:

A;Gene: PA5031  
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
Query Match 26.6%; Score 451; DB 2; Length 309;  
Best Local Similarity 39.2%; Pred. No. 2e-28;  
Matches 121; Conservative 37; Mismatches 121; Indels 30; Gaps 9;

QY 32 SKATIP---GKTVITGANTGIGKQTALALEARRGGNIILACRDMKCEAAAKDIRGETLN 88  
Db 5 TRRNIPQLAGRLALVTGANSGLGWQAARTLAGKGATVVMACRNREQAERARRAILDEYFQ 64  
QY 89 HHVNARHLDLASLKSIREFAAKIIEEERVDILINNAGVMRCPHWTTEDEGPEMQFGVNHL 148

Db 65 ARLELADLDLADLASIRACAAGFRQRRHARLDLLFNAGVMFLPLRRTRDGFEMQMGTNHL 124  
QY 149 GHFLLTNLLDKLKASAPSRRIINLSSLAHVAGHIDFDDLNWQTRKYNKTAAYCQSKLAIV 208  
Db 125 GHFALTGLLLDSLLAAPRPRVVGMTSGFNQFGRPLDLDLNAE-RGYNRYLAYCHSKQANL 183  
QY 209 LFTKELSRRLQSGVTVNAL--HPGVARTELGRHTGIHGSTFSSTTLGPIFWLL----- 260  
Db 184 LFSLELQRRAGQRGVLLQSLAAHPGYAATNL-----QYAAPAMSGSRLGR--WAMKVANGA 237  
QY 261 -VKSPELAAQPSSTYLAVAEELADVSGKYFD-----GLKQKAPAP-EAEDEEVARRLW 310  
Db 238 FAQSAEMGALPA--LSALTEQRWYGAYVGPDRWLETRGPYAAARIIPRNARDLGLAARLW 295  
QY 311 AESARLVGL 319  
Db 296 ALSEELTGV 304

RESULT 14  
T13447  
hypothetical protein T19F6.40 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 17-Mar-2000  
C:Accession: T13447; T13449  
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; New  
submitted to the Protein Sequence Database, July 1999  
A:Reference number: Z17587  
A:Accession: T13447  
A:Molecule type: DNA  
A:Residues: 1-332 <BEV>  
A:Cross-references: EMBL:AL109619; GSPDB:GN00062; ATSP:T19F6.40  
A:Experimental source: cultivar Columbia; BAC clone T19F6  
C:Genetics:  
A:Gene: ATSP:T19F6.40  
A:Map position: 4  
A:Introns: 41/1; 118/2; 145/1; 197/2; 224/3; 254/1; 269/3  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 26.4%; Score 447.5; DB 2; Length 332;  
Best Local Similarity 40.3%; Pred. No. 4.3e-28;  
Matches 118; Conservative 47; Mismatches 105; Indels 23; Gaps 9;  
QY 40 TVIVTGANTGIGKQTALRLARRGNNIILACRDMKCEAAAKDIRGETLNNHVNARHLDLA 99  
Db 36 TAVITGATSGIGAETARVLAKRGARLIFPARNVKAABEAKERIVSEFPETEIVVMKLDLS 95  
QY 100 SLKSIREFAAKIIEEERVDILINNAGVMRCPTHWTTEDCGFEMQFGVNHGHELLTNLLD 159  
Db 96 SIASVRNFVADFESLDPLNLLINNAGKLAHEHAISEDGIEMTFATNYLGHELLTNLLN 155  
QY 160 KL-----KASAPSRRIINLSSLAH--VAGH-IDFDDLNWQTR-KYNTKAAYCQSKLAIVLF 210  
Db 156 KMIQTAETGVQGRIVNVTSGIHGWFSGDLEYLRLISQPKQFDATRAYALSKLANVLH 215  
QY 211 TKELSRRLQ--GSGVTVNALHPGVARTELGR-HTGIHGSTFSSTTLGPIFWL---LVKSP 264  
Db 216 TKELSRRLQKIGANVTNVCVHPGVVTRLTRDREGL-----LTDL--VFPLASKLVKTV 267  
QY 265 ELAAQPSSTYLAVAEELADVSGKYFDGLKQKAPAEAEDEEVARRLWAEARLV 317  
Db 268 PQAAATTCYVATNPRLNVNVSCKYFDCNETTPSGLGTNSSEATKLWAASEILV 320

RESULT 15  
AE3195  
dehydrogenase Atu5290 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) plasmid  
C:Species: Agrobacterium tumefaciens  
C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002  
C:Accession: AE3195  
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McCell  
; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001  
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A;Reference number: AB2577; MUID:21608550; PMID:11743193  
A;Accession: AE3195  
A;Status: preliminary  
A:Molecule type: DNA  
A;Residues: 1-301 <KUR>  
A:Cross-references: GB:AE008687; PIDN:AAL45979.1; PID:g17743732; GSPDB:GN00188  
A;Experimental source: strain C58 (Dupont)  
C:Genetics:  
A:Gene: Atu5290  
A:Genome: plasmid  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.9%; Score 438.5; DB 2; Length 301;  
Best Local Similarity 38.2%; Pred. No. 2e-27;  
Matches 117; Conservative 52; Mismatches 110; Indels 27; Gaps 11;  
QY 32 SKATIP--GKTVIVTGANTGIGKQTALRLARRGNNIILACRDMKCEAAAKDIRGETLN 88  
Db 5 TEANIPNQRGRSAVVVTGTG-GLGLETALALARAGCDVTIAGRNPEKGSDAVSRIQRAAPH 63  
QY 89 HHVNARHLDLASLKSIREFAAKIIIEEERVDILINNAGVMRCP-HWTTEDGFEMQFGVNH 147  
Db 64 VTVSFEKLDLADLTSLALFAQRMENDRESLDLLVNNAGIMVPPKQRTDGFELQFGTNY 123  
QY 148 LGHFLLTNLLDKLKASAPSRRIINLSSLAHVAGHIDFDDLNWQTRKYNKTAAYCQSKLAI 207  
Db 124 LGHFALTALHMLPLLLKKGTDARVVTVSSVAARAGKINFADIN-SEKNYHPMRAYSQSKLAC 182  
QY 208 VLFTKELS--RRLQSGVTVNALHPGVARTELGRHTGIHGSTFSSTTLG---PIFWLLVK 262  
Db 183 LMFALQLQDRSRAAGWGVSSIAAHPGVSRDTL-----LHNAPGRNSLQGLARTPLWFLFQ 237  
QY 263 SPELAAQPSSTYLAVAEELADVSGKYF--DGLKQ-----KAPA---PEAEDEEVARRLWAE 313  
Db 238 PVAQGALPQLFSATSKEVK--SGGYGPDRLGETRGRHPQPARIPPEALDRVAGKQLWEIS 295  
QY 314 ARLVGL 319  
Db 296 QRMTGL 301

Search completed: June 23, 2004, 11:09:00  
Job time : 22 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.  
OM protein - protein search, using sw model  
Run on: June 23, 2004, 11:03:04 ; Search time 17 Seconds  
(without alignments)  
1013.837 Million cell updates/sec  
Title: US-10-015-393A-116  
Perfect score: 1695  
Sequence: 1 MSRYLLPLSALGTVAGAAVL.....ESARLVGLEAPSVREQLPLR 331  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 141681 seqs, 52070155 residues  
Total number of hits satisfying chosen parameters: 141681  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1688	99.6	331	1 RDHD_HUMAN	Q8nbn7 homo sapien
2	1443.5	85.2	334	1 RDHD_MOUSE	Q8cee7 mus musculu
3	739.5	43.6	318	1 RDHB_HUMAN	Q8tc12 homo sapien
4	738.5	43.6	316	1 RDHC_MOUSE	Q8byk4 mus musculu
5	737.5	43.5	316	1 RDHC_HUMAN	Q96nr8 homo sapien
6	730.5	43.1	316	1 RDHB_MOUSE	Q9qyf1 m retinol d
7	726	42.8	336	1 RDHE_HUMAN	Q9hbh5 homo sapien
8	722.5	42.6	334	1 RDHE_MOUSE	Q9eri6 mus musculu
9	714	42.1	316	1 RDHC_BOVIN	P59837 bos taurus
10	532	31.4	330	1 DHSX_HUMAN	Q8n5i4 homo sapien
11	408.5	24.1	280	1 DHSX_MOUSE	Q8vzb0 mus musculu
12	364.5	21.5	398	1 POR_DAUCA	Q9sdt1 daucus caro
13	356	21.0	397	1 POR_CHLRE	Q39617 chlamydomon
14	353.5	20.9	298	1 OXIR_STRAT	Q03326 streptomyc
15	352	20.8	297	1 OXIR_STRLI	P35320 streptomyc
16	346.5	20.4	405	1 POR_ARATH	Q42536 arabidopsis
17	345.5	20.4	399	1 POR_PEA	Q01289 pisum sativ
18	342	20.2	388	1 POR_HORVU	P13653 hordeum vul
19	339	20.0	388	1 POR_WHEAT	Q41578 triticum ae
20	338.5	20.0	401	1 PORB_ARATH	P21218 arabidopsis
21	338	19.9	398	1 PORA_CUCSA	Q41249 cucumis sat
22	336	19.8	322	1 POR_FLEBO	Q66148 plectonema
23	331	19.5	313	1 POR_AVEA	P15904 avena sativ
24	329	19.4	401	1 PORC_ARATH	Q48741 arabidopsis
25	326.5	19.3	395	1 PORB_HORVU	Q42850 hordeum vul
26	325	19.2	322	1 POR_SYNY3	Q59987 synchocyst
27	310.5	18.3	458	1 POR_MARPA	Q80333 marchantia
28	289	17.1	407	1 YNSI_YEAST	P53878 saccharomyc
29	242.5	14.3	267	1 YM71_YEAST	Q05016 saccharomyc
30	237.5	14.0	263	1 UCPA_SALTY	P37441 salmonella
31	229.5	13.5	246	1 FABG_THEMEA	Q9x248 thermotoga
32	222.5	13.1	263	1 UCPA_ECO57	Q8xbj4 escherichia
33	222.5	13.1	263	1 UCPA_ECOLI	P37440 escherichia

ALIGNMENTS

RESULT 1

ID	RDHD_HUMAN	STANDARD;	PRT;	331 AA.
AC	Q8NBN7;			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Retinol dehydrogenase 13 (EC 1.1.1.-).			
GN	RDH13.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Teratocarcinoma;			
RA	Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,			
RA	Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,			
RA	Nagahari K., Sugano S., Isogai T.;			
RT	"HRI human cDNA sequencing project.";			
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBSJ databases.			
RN	[2]			
RP	TISSUE SPECIFICITY, AND ENZYMATIC ACTIVITY.			
RX	MEDLINE=22323226; PubMed=12226107;			
RA	Haeseleer F., Jang G.-F., Imanishi Y., Driessen C.A.G.G.,			
RA	Matsumura M., Nelson P.S., Palczewski K.;			
RT	"Dual-substrate specificity short chain retinol dehydrogenases from			
RT	the vertebrate retina.";			
RL	J. Biol. Chem. 277:45537-45546(2002).			
CC	-!- FUNCTION: Does not exhibit retinol dehydrogenase (RDH) activity in			
CC	vitro.			
CC	-!- TISSUE SPECIFICITY: Expressed mostly in eye, pancreas, placenta			
CC	and lung. In the retina, detected in the inner segment of the			
CC	photoreceptor cells. Weak signals were observed in a small			
CC	population of inner nuclear neurons and the inner plexiform layer.			
CC	-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases			
CC	(SDR) family.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AK075392; BAC11591.1; --			
DR	Genew; HGNC:19978; RDH13.			
DR	InterPro; IPR002198; ADH_short.			
DR	Pfam; PF00106; adh_short; 1.			
DR	PRINTS; PR00080; SDRFAMILY.			
DR	PROSITE; PS00061; ADH_SHORT; 1.			
KW	Oxidoreductase; NADP.			
FT	NP_BIND 45 51 NAD OR NADP (BY SIMILARITY).			
FT	ACT_SITE 200 200 BY SIMILARITY.			
FT	SEQUENCE 331 AA; 35902 MW; E84A3759D2D274F5 CRC64;			
SQ				

P16542 streptomyc  
P51831 bacillus su  
Q10402 mycobacteri  
P73574 synchocyst  
P50941 rickettsia  
O67610 aquifex aeo  
Q9WY90 thermotoga  
Q92247 neospora  
P28643 cuphea lanc  
Q45219 bradyrhizob  
Q9rpt1 pseudomonas  
Q9kqh7 vibrio chol

Query Match 99.6%; Score 1688; DB 1; Length 331;  
Best Local Similarity 99.7%; Pred. No. 2.8e-130;  
Matches 330; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTIVITGANTGIGKQTALRLAR 60  
DB 1 MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTIVITGANTGIGKQTALRLAR 60

QY 61 RGGNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASKSIREFAAKIIEEERVDI 120  
DB 61 RGGNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASKSIRVFAAKIIEEERVDI 120

QY 121 LINNAGVMRCPHWTTEDEGFEMQGVNHLGHFLTNLLDCLKASAPSRINISSLAHVAG 180  
DB 121 LINNAGVMRCPHWTTEDEGFEMQGVNHLGHFLTNLLDCLKASAPSRINISSLAHVAG 180

QY 181 HIDFDDLNWQTRKYNNTKAAVQSKLAIVLFTKELSRRLQSGVTVNALHPGVARTLGRH 240  
DB 181 HIDFDDLNWQTRKYNNTKAAVQSKLAIVLFTKELSRRLQSGVTVNALHPGVARTLGRH 240

QY 241 TGIHGTSFSTTLGPIFWLLVKSPELAAPSTYLAVAEELADVSGKYFDGLKQKAPAPEA 300  
DB 241 TGIHGTSFSTTLGPIFWLLVKSPELAAPSTYLAVAEELADVSGKYFDGLKQKAPAPEA 300

QY 301 EDEVARRLWAESARLVGLEAPSVREQPLPR 331  
DB 301 EDEVARRLWAESARLVGLEAPSVREQPLPR 331

RESULT 2  
RDHD\_MOUSE  
ID RDHD\_MOUSE STANDARD; PRT; 334 AA.

AC Q8CEE7; Q8CC07;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Retinol dehydrogenase 13 (EC 1.1.1.-).  
GN RDH13.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Diencephalon, and Liver;  
RX MEDLINE=22354683; PubMed=12466851;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustircich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Sempole C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
CC -!- FUNCTION: Does not exhibit retinol dehydrogenase (RDH) activity  
CC in vitro (By similarity).  
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases  
CC (SDR) family.  
CC  
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CC or send an email to license@isb-sib.ch).  
CC  
CC EMBL; AK028434; BAC25950.1; -.  
CC EMBL; AK034180; BAC28618.1; -.  
CC MGD; MGI:1918732; Rdh13.  
CC InterPro; IPR002198; ADH\_short.  
CC Pfam; PF00106; adh\_short; 1.  
CC PRINTS; PR00080; SDRFAMILY.  
CC PROSITE; PS00061; ADH\_SHORT; 1.  
KW Oxidoreductase; NADP.  
FT NP BIND 45 51 NAD OR NADP (BY SIMILARITY).  
FT ACT SITE 200 200 BY SIMILARITY.  
FT CONFLICT 114 148 MISSING (IN REF. 1; BAC28618).  
SQ SEQUENCE 334 AA; 36464 MW; 4EBBCE1643C1FECE CRC64;

Query Match 85.2%; Score 1443.5; DB 1; Length 334;  
Best Local Similarity 83.6%; Pred. No. 2.4e-110;  
Matches 280; Conservative 21; Mismatches 29; Indels 5; Gaps 2;

QY 1 MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTIVITGANTGIGKQTALRLAR 60  
DB 1 MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTIVITGANTGIGKQTALRLAR 60

QY 61 RGGNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASKSIREFAAKIIEEERVDI 120  
DB 61 RGGNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASKSIREFAAKIIEEERVDI 120

QY 121 LINNAGVMRCPHWTTEDEGFEMQGVNHLGHFLTNLLDCLKASAPSRINISSLAHVAG 180  
DB 121 LINNAGVMRCPHWTTEDEGFEMQGVNHLGHFLTNLLDCLKASAPSRINISSLAHVAG 180

QY 181 HIDFDDLNWQTRKYNNTKAAVQSKLAIVLFTKELSRRLQSGVTVNALHPGVARTLGRH 240  
DB 181 HIDFDDLNWQTRKYNNTKAAVQSKLAIVLFTKELSRRLQSGVTVNALHPGVARTLGRH 240

QY 241 TGIHGTSFSTTLGPIFWLLVKSPELAAPSTYLAVAEELADVSGKYFDGLKQKAPAPEA 300  
DB 241 TGMHNSAFSGFMLGPFLLFKSPQLAASPSTYLAVAEELADVSGKYFDGLREKAPSPEA 300

QY 301 EDEVARRLWAESARLVGLEAPSVREQPLPR 331  
DB 301 EDEVARRLWAESARLVGLEAPSVREQPLPR 331

RESULT 3  
RDHB\_HUMAN  
ID RDHB\_HUMAN STANDARD; PRT; 318 AA.  
AC Q8TC12; Q9NRW0; Q9Y391;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Retinol dehydrogenase 11 (EC 1.1.1.-) (Retinal reductase 1) (Ralr1)  
DE (Prostate short-chain dehydrogenase/reductase 1) (Androgen-regulated  
DE short-chain dehydrogenase/reductase 1) (HCV core-binding protein  
DE HCBP12) (CGI-82).  
GN RDH11 OR PSDR1 OR ARSDR1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.





Db 310 CDLLGL 315

RESULT 4

RDHC MOUSE STANDARD; PRT; 316 AA.

AC Q8BYK4; Q91WA5; Q9D1Y4;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Retinol dehydrogenase 12 (EC 1.1.1.-).

GN RDH12.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Spinal cord;

RX MEDLINE=22354683; PubMed=12466851;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,

RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573 (2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Retina;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodriques S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -!- FUNCTION: Exhibits an oxidoreductive catalytic activity towards

CC retinoids. Most efficient as an NADPH-dependent retinal reductase.

CC Displays high activity toward 9-cis and all-trans-retinol. Also

CC involved in the metabolism of short-chain aldehydes. No steroid

CC dehydrogenase activity detected. Might be the key enzyme in the

CC formation of 11-cis-retinal from 11-cis-retinol during

CC regeneration of the cone visual pigments (By similarity).

CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases

CC (SDR) family.

CC -----

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CC -----

DR EMBL; AK020927; BAB32258.1; -.

DR EMBL; AK039233; BAC30288.1; -.

DR EMBL; BC016204; AAHL6204.1; -.

DR MGD; MGI:1925224; Rdh12.

DR InterPro; IPR002198; ADH\_short.

DR Pfam; PF00106; adh\_short; 1.

DR PRINTS; PR00080; SDRFAMILY.

DR PROSITE; PS00061; ADH\_SHORT; FALSE\_NEG.

KW Oxidoreductase; NADP; Vision.

FT NP BIND 46 52 NADP (BY SIMILARITY).

FT ACT SITE 200 200 BY SIMILARITY.

FT CONFLICT 114 125 MISSING (IN REF. 2).

FT CONFLICT 120 120 H -> D (IN REF. 1; BAB32258).

SQ SEQUENCE 316 AA; 35292 MW; CF5745B6710A6148 CRC64;

Query Match 43.6%; Score 738.5; DB 1; Length 316;

Best Local Similarity 48.7%; Pred. No. 7.1e-53;

Matches 154; Conservative 56; Mismatches 99; Indels 7; Gaps 2;

QY 5 LLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVITGANTGIGKQTALELARRGN 64

Db 6 VLTSLFLSILYLTAPSIRKFFAGGVCTTNVQIPGVVITGANTGIGKETARELARRGAR 65

QY 65 IILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEERVDILNN 124

Db 66 VYIACRDVLKGESAASEIRADTKNSQVLVRKLDLSDTKSIRAFERFLAEKHLILNN 125

QY 125 AGVMRCPHWTTEDEGFEMQFGVNHGLHFLTLNLLDLKLKASAPSRRIINLSSLAHVAGHIDF 184

Db 126 AGVVMCPYSKTTDGFETHFGVNHGLHFLTLNLLERLKSAPARVNVNLSIAHLGKIRF 185

QY 185 DDLNMQTRKYNTKAAAYCQSKLAIVLFTKELSRRLQSGVTVNALHPGVARTELGRHTGIH 244

Db 186 HDLQOQ-KRYCSAFAYGHSKLANLLFTRELAKRLQGTGTAYAVHPGVVLSEITR----- 239

QY 245 GSTFSSSTLGPFIWLLVKSPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAEAEDEE 304

Db 240 -NSYLLCLLWRLFSPPFKSTSQGAQTSLHCALEADLEPLSGKYFSDCKRMWVSSRARNKK 298

QY 305 VARRLWAFESARLVGLE 320

Db 299 TAERLWNVSCCELLGIQ 314

RESULT 5

RDHC\_HUMAN

ID RDHC\_HUMAN STANDARD; PRT; 316 AA.

AC Q96NR8; Q8TAW6;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Retinol dehydrogenase 12 (EC 1.1.1.-).

GN RDH12.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;















FT NP BIND 47 71 NAD OR NADP (BY SIMILARITY).  
FT ACT\_SITE 208 208 BY SIMILARITY.  
FT DOMAIN 157 163 POLY-LEU.  
FT NON\_TER 280 280  
SQ SEQUENCE 280 AA; 30203 MW; 2A34C9A485CAE632 CRC64;  
  
Query Match 24.1%; Score 408.5; DB 1; Length 280;  
Best Local Similarity 40.4%; Pred. No. 5e-26;  
Matches 112; Conservative 32; Mismatches 122; Indels 11; Gaps 5;  
  
QY 3 RYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVITGANTGIGKQTALRLARRG 62  
Db 8 RAVLCVYAVGIAVALAQLLRRLRGDFRPPVLPPOPGRVAIVTGATAGIGRSTARQLARLG 67  
  
QY 63 GNIILACRDMKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEERVDILI 122  
Db 68 MCVVAGNDEHRGQEVVSSIRAEVSGDRAHFLPLDLASLASVGRGFARDFOALGLPLHLV 127  
  
QY 123 NNAGVMRCPHWTTEDEGFEMQFQVNVHLGHFLTLNLLDKLKASAP----SRIINLSSLAHV 178  
Db 128 NNAVMLEPRAETEDGFERHLGVNFLGHFLTLNLLPALRASGAEGRSRVTVGSATQY 187  
  
QY 179 AGHIDFDDLNWQTRKYNKTAAYCQSKLAIVLFTKELSRRL--QSGVTVNALHPGVARTE 236  
Db 188 VGTVDMAHLGR-HAYSPYAAYAQSKLALFALQLQRLDARGDPVTSNMADPGVVDTE 246  
  
QY 237 LGRHTGHSSTTTLGPIFWLLVKSPELAAQPSY 273  
Db 247 MYRHAGVLR-TAKRFLG---WLVFKEEGAWTLVY 279  
  
RESULT 12  
POR\_DAUCA  
ID POR DAUCA STANDARD; PRT; 398 AA.  
AC Q9SDT1;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Protochlorophyllide reductase, chloroplast precursor (EC 1.3.1.33)  
DE (PCR) (NADPH-protochlorophyllide oxidoreductase) (POR).  
GN POR1.  
OS Daucus carota (Carrot).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
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OC Daucus.  
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RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Kurodagosun;  
RA Sato K., Demura T., Fukuda H.;  
RT "Cloning of photosynthesis-related genes and their expression during  
RT somatic embryogenesis in carrot."  
RL Plant Cell Physiol. 38:77-77(1997).  
CC -!- FUNCTION: Phototransformation of protochlorophyllide (Pchl) to  
CC chlorophyllide (Chlide).  
CC -!- CATALYTIC ACTIVITY: Chlorophyllide A + NADP(+) =  
CC protochlorophyllide + NADPH.  
CC -!- PATHWAY: Chlorophyll biosynthesis.  
CC -!- SUBCELLULAR LOCATION: Chloroplast.  
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases  
CC (SDR) family. POR subfamily.  
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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DR EMBL; AF207691; AAF20949.1; --  
DR HSSP; P14061; 1FDU.

DR InterPro; IPR002198; ADH\_short.  
DR InterPro; IPR005979; Prochl\_reduct.  
DR Pfam; PF00106; adh\_short; 1.  
DR TIGRFAMs; TIGR01283; LPOR; 1.  
KW Photosynthesis; Chlorophyll biosynthesis; Oxidoreductase; NADP;  
KW Chloroplast; Transit peptide.  
FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).  
FT CHAIN ? 398 PROTOCHLOROPHYLLIDE REDUCTASE.  
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Matches 121; Conservative 48; Mismatches 134; Indels 49; Gaps 15;  
  
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DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Protochlorophyllide reductase, chloroplast precursor (EC 1.3.1.33)  
DE (PCR) (NADPH-protochlorophyllide oxidoreductase) (POR).  
GN PORA OR LPCR-1.  
OS Chlamydomonas reinhardtii.  
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RA Li J., Timko M.P.;  
RT "The pc-1 phenotype of Chlamydomonas reinhardtii results from a  
RT deletion mutation in the nuclear gene for NADPH:protochlorophyllide  
RT oxidoreductase."  
RL Plant Mol. Biol. 30:15-37(1996).  
CC -!- FUNCTION: Phototransformation of protochlorophyllide (Pchl) to  
CC chlorophyllide (Chlide).  
CC -!- CATALYTIC ACTIVITY: Chlorophyllide A + NADP(+) =  
CC protochlorophyllide + NADPH.  
CC -!- PATHWAY: Chlorophyll biosynthesis.  
CC -!- SUBCELLULAR LOCATION: Chloroplast.  
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases  
CC (SDR) family. POR subfamily.  
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Search completed: June 23, 2004, 11:08:27  
Job time : 19 secs





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AC011476/c

LOCUS

DEFINITION

AC011476

AC011476

AC011476.8

HTG

Source

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www.shgc.stanford.edu

Quality: Phrap Quality >=40 99.9% of Sequence;

Estimated Total Number of Errors is 0.3.

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copies 67315-69359. Unsure number of repeat copies 67315-69359.

NOTE: Shatter libraries failed to resolve dinucleotide repeat

region 171590-171722. Unsure number of repeat copies

171590-171722. Forced join 171695.

Location/Qualifiers

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/chromosome="19"

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ORIGIN

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Matches 965; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 148056 GGGCCCATCTTCTGGCTGCTGCTCAAGAGCCCGAGCTGGCGGCCAGCACATAC 147997

QY 901 CTGGCCGTGGCGGAGGAACCTGGCGGATGTTCCGGAAGTACTTCGATGGACTCAACAG 960

Db 147996 CTGGCCGTGGCGGAGGAACCTGGCGGATGTTCCGGAAGTACTTCGATGGACTCAACAG 147937

QY 961 AAGGCCCGCCCCCGAGGCTGAGGATGAGGAGGTGGCCCGAGGCTTTGGGCTGAAAGT 1020

Db 147936 AAGGCCCGCCCCCGAGGCTGAGGATGAGGAGGTGGCCCGAGGCTTTGGGCTGAAAGT 147877

QY 1021 GCCCGCCTGGTGGGCTTAGAGGCTCCCTCTGTGAGGAGCAGCCCTCCCCAGATAACCT 1080

Db 147876 GCCCGCCTGGTGGGCTTAGAGGCTCCCTCTGTGAGGAGCAGCCCTCCCCAGATAACCT 147817

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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(without alignments)  
10449.989 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: geneseqn1990s:\*\*  
3: geneseqn2000s:\*\*  
4: geneseqn2001as:\*\*  
5: geneseqn2001bs:\*\*  
6: geneseqn2002s:\*\*  
7: geneseqn2003as:\*\*  
8: geneseqn2003bs:\*\*  
9: geneseqn2003cs:\*\*  
10: geneseqn2004s:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1808	100.0	1808	8	ACH04423 Human CDN
5	1808	100.0	1808	8	ACD67967 Novel hum
6	1808	100.0	1808	9	ADC17984 Human PRO
7	1808	100.0	1808	9	ADD70630 Human CDN
8	1808	100.0	1808	9	ADD39707 Human CDN
9	1808	100.0	1808	9	ADD70153 Human CDN
10	1808	100.0	1808	9	ADD38274 Human CDN
11	1808	100.0	1808	9	ADD39230 Human CDN
12	1808	100.0	1808	9	ADD38753 Human CDN
13	1808	100.0	1808	9	ADD40184 Human CDN
14	1808	100.0	1808	9	ADE50405 Human CDN
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16	1808	100.0	1808	9	ADE49928 Human CDN
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19	1792	99.1	1878	5	AAF93783 Human CDN
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ALIGNMENTS

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XX 08-AUG-2000 (first entry)

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XX Human; PRO polypeptide; membrane bound protein; receptor; diagnosis; transmembrane; secretion; immunoadhesion; pharmaceutical; screening; ss.

XX Homo sapiens.

XX WO200012708-A2.

XX 09-MAR-2000.

XX 01-SEP-1999; 99WO-US020111.

XX 01-SEP-1998; 98US-0098716P.

XX 01-SEP-1998; 98US-0098749P.

XX 01-SEP-1998; 98US-0098750P.

XX 02-SEP-1998; 98US-0098803P.

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XX 02-SEP-1998; 98US-0098843P.

XX 09-SEP-1998; 98US-0099536P.

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PR 18-NOV-1998; 98US-0108904P.
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(GETH ) GENENTECH INC.

Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;

WPI; 2000-237871/20.  
P-PSDB; AAY99372.

New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions.

Claim 2; Fig 65; 773pp; English.

AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents: AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention

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Qy 61 GACGCTGTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
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Db 61 GACGCTGTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120

Qy 121 GTAGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
    |||||
Db 121 GTAGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180

Qy 181 GCCACCATCCCTGGGAAGACGGTCTATGTCAGGAGCTATGTCACGGTGGGGCTTCCCCAGCAAG 240
    |||||
Db 181 GCCACCATCCCTGGGAAGACGGTCTATGTCAGGAGCTATGTCACGGTGGGGCTTCCCCAGCAAG 240

Qy 241 ACCGCTTGGAACTGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
    |||||
Db 241 ACCGCTTGGAACTGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
```

## Sequence Comparison

QY	301	AAGTGTGAGCGGCAGCAAAGGACATCCGCGGGAGACCCCTCAATCACCATTGTCAACGCC	360
DB	301	AAGTGTGAGCGGCAGCAAAGGACATCCGCGGGAGACCCCTCAATCACCATTGTCAACGCC	360
QY	361	CGGCACCTGGACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAAGATCATTTGAA	420
DB	361	CGGCACCTGGACTTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAAGATCATTTGAA	420
QY	421	GAGGAGGAGCGAGTGGACATTTCTAATCAACAAACGCGGGTGTGATGCGGTGCCCCACTGG	480
DB	421	GAGGAGGAGCGAGTGGACATTTCTAATCAACAAACGCGGGTGTGATGCGGTGCCCCACTGG	480
QY	481	ACCACCGAGGACGGCTTCGAGATGCAGTTTGGCGTTTAAACACCTGGGTCACTTTCTCTTG	540
DB	481	ACCACCGAGGACGGCTTCGAGATGCAGTTTGGCGTTTAAACACCTGGGTCACTTTCTCTTG	540
QY	541	ACAAACTTGTCTGGACAAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCG	600
DB	541	ACAAACTTGTCTGGACAAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCG	600
QY	601	TCCCTGGCCCCATGTTGCTGGGCACATAGACTTTGACGACTTGAACCTGGCAGACGAGGAAG	660
DB	601	TCCCTGGCCCCATGTTGCTGGGCACATAGACTTTGACGACTTGAACCTGGCAGACGAGGAAG	660
QY	661	TATAACACCAAAGCCGCTACTGCCAGAGCAAGCTCGCCATCGTCTCTTCAACCAAGSAG	720
DB	661	TATAACACCAAAGCCGCTACTGCCAGAGCAAGCTCGCCATCGTCTCTTCAACCAAGSAG	720
QY	721	CTGAGCCGGCGGCTGCAAGGCTCTGGTGTGACTGTCAACGSCCTGCACCCCGCGTGSCT	780
DB	721	CTGAGCCGGCGGCTGCAAGGCTCTGGTGTGACTGTCAACGSCCTGCACCCCGCGTGSCT	780
QY	781	AGGACAGAGCTGGGCAGACACACGGGCATCCATGGCTCCACCTTCTCCAGCACCACTC	840
DB	781	AGGACAGAGCTGGGCAGACACACGGGCATCCATGGCTCCACCTTCTCCAGCACCACTC	840
QY	841	GGSCCCATCTTCTGGCTGCTGGTCAAGAGCCCCGAGCTGGSCGCCCCAGCCAGCATAC	900
DB	841	GGSCCCATCTTCTGGCTGCTGGTCAAGAGCCCCGAGCTGGSCGCCCCAGCCAGCATAC	900
QY	901	CTGGCCGTGGCGAGGAACCTGGCGGATGTTTCGGAAAGTACTTCGATGGACTCAAACAG	960
DB	901	CTGGCCGTGGCGAGGAACCTGGCGGATGTTTCGGAAAGTACTTCGATGGACTCAAACAG	960
QY	961	AAGGCCCGGCCCCCGAGGCTGAGGATGAGGAGTGGCCGAGGCTTTGGGCTGAAGT	1020
DB	961	AAGGCCCGGCCCCCGAGGCTGAGGATGAGGAGTGGCCGAGGCTTTGGGCTGAAGT	1020
QY	1021	GCCCGCTGTGGGCTTAGAGGCTTCCCTCTGTGAGGAGAGCCCTCCCGAGATAACCT	1080
DB	1021	GCCCGCTGTGGGCTTAGAGGCTTCCCTCTGTGAGGAGAGCCCTCCCGAGATAACCT	1080
QY	1081	CTGGAGCAGATTTGAAAGCCAGGATGGCGCTCCAGACCGAGGACAGCTGTCCGCCATGC	1140
DB	1081	CTGGAGCAGATTTGAAAGCCAGGATGGCGCTCCAGACCGAGGACAGCTGTCCGCCATGC	1140
QY	1141	CCGAGCTTCCCTGGCACTACCTGAGCCGGGAGACCCAGGACTGGCGGCCCATGCCCCG	1200
DB	1141	CCGAGCTTCCCTGGCACTACCTGAGCCGGGAGACCCAGGACTGGCGGCCCATGCCCCG	1200
QY	1201	AGTAGGTTCTAGGGGGCGGTGCTGGCCGACGTGGACTGGCCTGCAGGTGAGCATGCCCC	1260
DB	1201	AGTAGGTTCTAGGGGGCGGTGCTGGCCGACGTGGACTGGCCTGCAGGTGAGCATGCCCC	1260
QY	1261	GGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAGAGGGCCATCTGATGCTT	1320
DB	1261	GGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAGAGGGCCATCTGATGCTT	1320
QY	1321	CCCTGGGAATCTAACTGGGAATGGCCGAGGAGGAAGGGCTCTGTGCACTTGCAGGCC	1380
DB	1321	CCCTGGGAATCTAACTGGGAATGGCCGAGGAGGAAGGGCTCTGTGCACTTGCAGGCC	1380

## RESULT 2

AAE54284

AAF54284  
ID AAF54284 standard; DNA; 1808 BP.

AC AAF54284;

XX  
DT 02-APR-2001 (first entry)

XX DE DNA encoding protein of th

DE DNA encoding protein of the invention #33.

Secreted; transmembrane; gene therapy; ss.

XX OS Unidentified.

XX PN WO200078961-A1.

PD 28-DEC-2000.

XX  
PF 18-FEB-2000; 2000WO-US004342.

AA 23-JUN-1999; 99US-0141037P.

PR 20-JUL-1999; 99US-0144758P.

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EX	18-DEC-1999;	39WO-US030093.
PR	05-JAN-2000;	2000WO-US000219.

PR 06-JAN-2000; 2000WO-US0000376.

XX DA (GETH ) GENENTECH INC

FA (GETH) GENENTECH INC.  
XX

PA (GETH ) GENENTECH INC.

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;

PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NE, Roy MA, Smith V, Stewart TA, Thomas D, Watanabe CK;

PI Williams PM, Wood WI;  
 FI Fair O, Fackell NF, Roy RA, Smith V, Stewart IA, Tullas D, Watcann CN;

















DR WPI; 2001-071395/08.  
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